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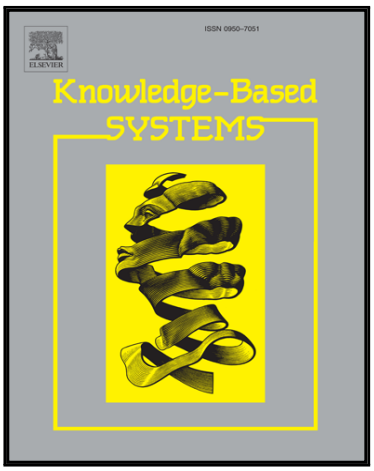

An Efficient Binary Salp Swarm Algorithm with Crossover Scheme for Feature Selection Problems

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Highlights

- Two wrapper feature selection approaches using salp swarm algorithm are proposed.
- The crossover operator is utilized in addition to transfer functions to enhance the algorithm.
- The performance is evaluated based on 22 datasets, and compared to five well-known wrapper methods.

An Efficient Binary Salp Swarm Algorithm with Crossover Scheme for Feature Selection Problems

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Abstract

Searching for the (near) optimal subset of features is a challenging problem in the process of Feature Selection (FS). In the literature, Swarm Intelligence (SI) algorithms show superior performance in solving this problem. This motivated our attempts to test the performance of the newly proposed Salp Swarm Algorithm (SSA) in this area. As such, two new wrapper FS approaches that use SSA as the search strategy are proposed. In the first approach, eight transfer functions are employed to convert the continuous version of SSA to binary. In the second approach, the crossover operator is used in addition to the transfer functions to replace the average operator and enhance the exploratory behavior of the algorithm. The proposed approaches are benchmarked on 22 well-known UCI datasets and the results are compared with 5 FS methods: Binary Grey Wolf Optimizer (BGWO), Binary Gravitational Search Algorithms (BGSA), Binary Bat Algorithm (BBA), Binary Particle Swarm Optimization (BPSO), and Genetic Algorithm (GA). The paper also considers an extensive study of the parameter setting for the proposed technique. From the results, it is observed that the proposed approach significantly outperforms others on around 90% of the datasets.

Keywords: Wrapper Feature Selection, Salp Swarm Algorithm, Optimization, Classification

1. Introduction

Dimensionality is the main challenge that may degrade the performance of the machine learning tasks (e.g., classification). There are many applications in science and engineering fields like medicine, biology, industry, etc. that depend on high dimensional datasets with hundreds or even thousands of features, and some of these features are irrelevant, redundant or noisy [1]. The existence of such features in the dataset may mislead the learning algorithm or cause data over-fit [2]. Feature Selection (FS) is an important pre-processing step

that aims to eliminate those types of features to enhance the effectiveness of the learning algorithms (e.g., classification accuracy) and save resources (e.g., CPU time and memory requirement).

FS methods are categorized based on the involvement of a learning algorithm in the selection process. Filter methods (Chi-Square [3], Information Gain [4], Gain Ratio [5], ReliefF [6]) rely on some data properties without involving a specific learning algorithm. On the other hand, wrapper methods depend on a specific learning algorithm (e.g. classifier) in evaluating the selected subset of features [7]. Comparing these families, wrappers are more accurate since they consider the relations between the features themselves. However, they are computationally more expensive than filters and their performances are strongly depend on the employed learning algorithm [8].

Searching for the (near) optimal subset of features is another key issue that must be taken into consideration when designing a FS algorithm. FS is considered as an NP-complete combinatorial optimization problem [9]. Hence, generating all possible subsets using techniques such as brute-force or exhaustive search strategy is impractical. Suppose that a dataset includes N features, then 2^N subsets are to be generated and evaluated [10], which is considered as a computationally expensive task especially in the wrapper based methods where the learning algorithm will be executed for each subset.

Since the main aim in FS is to minimize the number of selected features while maintaining the maximum classification accuracy (i.e., minimize the classification error rate), it can be considered as an optimization task. Therefore, metaheuristics, which showed superior performance in solving different optimization scenarios, are potentially suitable solutions for FS problems [11].

Swarm Intelligence (SI) techniques are nature-inspired metaheuristics algorithms that mimic the swarming behavior of ants, bees, schools of fish, flocks of birds, herds of land animals, etc. that live in groups in nature and can cooperate among themselves [12]. Examples of SI algorithms include but not limited to Particle Swarm Optimization (PSO) [13], Ant Colony Optimization (ACO) [14], Dragonfly Algorithm (DA) [15], Whale Optimization Algorithm (WOA) [16], Water Cycle Algorithm (WCA) [17, 18], Krill Herd (KH) [19] algorithm, Fruit Fly Optimization Algorithm (FFOA) [20], Grey Wolf Optimizer (GWO) [21], and Firefly Algorithm (FA) [22]. These algorithms were used in solving many optimization problems including feature selection problems and showed superior performance when compared to several exact methods [10, 23]. For details about the history of metaheuristics, interested readers can refer to [24].

SSA is a recent SI optimizer proposed by Mirjalili *et al.* [25]. SSA mimics the swarming behaviour of salps when navigating and foraging in oceans. It was shown in [25] that SSA significantly outperforms well-regarded and recent metaheursitics. This is due to the several stochastic operators integrated into SSA that allows this algorithm to better avoid local solutions in multi-modal search landscapes. Mirjalili *et al.* also showed that the SSA algorithm performs efficiently on small- and large-scale problems. As a binary problem with a large number of local solutions, the number of parameters of a feature selection problem varies significantly when changing datasets that should be addressed by a reliable stochastic optimization algorithm. This motivated our attempts to propose a feature selection technique using SSA to benefit from the flexibility and highly stochastic nature of this algorithm in handling diverse range of parameter and local solutions.

In this paper, two FS approaches based on SSA are proposed. The native SSA was proposed to deal with continuous problems, so some modifications should be done on SSA to solve FS problems with binary parameters. Mainly, two versions of binary SSA are proposed in this work:

- In the first version, the SSA is converted from continuous to binary using eight different transfer functions (TFs).
- In the second version, a crossover operator is integrated to SSA. In fact, the best search agent of SSA (leader) is updated using the crossover operator to promote exploration while maintaining the main mechanism of this algorithm.

The structure of this paper is as follows: the review of related works is presented in Section 2. Section 3 presents some preliminaries and theoretical background about FS, k-NN classifier, and SSA algorithm utilized in this research. The new SSA-based techniques are proposed in Section 4. Section 5 represents the details of binary SSA for FS tasks. Section 6 reports the obtained results and related comparisons and discussions. Finally, the conclusion and several directions for future papers are presented in Section 7.

2. Review of related works

In literature, many SI algorithms have been extensively used as search strategies in wrapper FS methods to enhance the results of the classification problems, which are one of the most important data mining tasks. The authors in [26] proposed an ACO-based FS algorithm called (ABACO). A novel FS algorithm based on ABACO has been also proposed in [27] by the same authors. This approach differs from the previous one by giving ants the ability to view the features comprehensively, and helps them to select the most salient features. A hybrid algorithm between two SI algorithms (ACO and ABC) called (AC-ABC Hybrid) has been recently proposed in [28]. In this algorithm, the advantages of both ACO and BCO have combined to produce a better algorithm; the Bees adapt the feature subsets generated by the Ants as their food sources and the Ants use the Bees to determine the best feature subset. Another hybrid model between the ACO and GA has been proposed in [29].

The PSO is a dominant SI algorithm that has been widely used with FS problem. Moradi *et al.* [30] enhanced the performance of PSO by employing a local search to find the salient and less correlated feature subset. Another two different FS approaches based on PSO have been proposed in [31]. In these two approaches a new variable was added to the original PSO which makes it more effective in tackling the FS problem. The PSO for FS has been also utilized in different fields like text clustering [32, 33], text FS [34], disease diagnosis [31, 35]. A FS method using artificial bee colony (ABC) has been proposed for Image steganalysis problem in [36]. A novel ABC based FS approach called wBCO has been proposed in Moayedikia et al. [37]. Two SI based algorithms (namely differential evolution (DE) and ABC) combined in a hybrid FS method in [38]. The Ant Lion Optimizer (ALO) [39] has been employed as a search strategy in a wrapper FS method in [40]. Moreover, three variants of binary ALO algorithm has been presented in [41]. A modified ALO algorithm, where a set of chaotic maps was used to control the balance between exploration and exploitation, has been proposed for FS in [42].

The GWO is a successful SI algorithm that mimics the social hierarchy and hunting traits of the grey wolves [21, 43, 44, 45]. The GWO has successfully been applied to FS problems in a number of works [46, 47]. Moth-flame Optimisation (MFO) [48] also revealed a relatively satisfying efficacy on both optimization and feature selection tasks [42]. The Whale Optimization Algorithm (WOA)-based FS approaches has also been proposed in [49], in which different hybridization models between the WOA and Simulated Annealing (SA) algorithm have been proposed for FS problems. Moreover, many SI-based FS approaches have been proposed in literature such as Genetic Algorithm (GA)-based FS [50, 51, 52], Gravitational Search Algorithm (GSA) [53, 54], DE [55, 56], Harmony Search (HS) [57], Bat Algorithm (BA) [58], Binary Grasshopper Optimization Algorithm (BGOA) [59], Binary Firefly Algorithm (BFA) [60], Binary Harmony Search (BHS) [61], Binary Cuckoo Search (BCS) [62],Binary Charged System Search (BCSS) [63]. For more FS approaches, readers can refer to the available review studies [64, 65]. Referring to No-Free-Lunch (NFL) theorem [66], it can be stated that there is no algorithm that can be the best universal machine for tackling all classes of feature selection problems. Hence, there are many opportunities to propose new algorithms or develop new improved variants of previous algorithms to tackle feature selection problems more efficiently.

3. Preliminaries

3.1. Feature Selection for Classification

A dataset (also called training set) usually consists of rows (called objects) and columns (called features) associated with predefined classes (decision features). Classification is a primary task in data mining, it's main role is to to predict the class of an unseen object [64]. The main problem that may affect the the accuracy and the performance of a specific classifier is the large number of features in the dataset which may be redundant or irrelevant. According to [2], the redundant and irrelevant features may negatively affect the classifier's performance in many directions; more features in a dataset raises the need for more instances to be added which costs the classifier longer time to learn. Moreover, the classifier that learns from irrelevant features is less accurate than the one that learns form relevant features. This is because the irrelevant features may mislead the classifier and cause them to overfit data. In addition, the redundant and irrelevant data will increase the complexity of the classifier which make it hard to understand the learned results.

FS usually helps in determining the irrelevant and redundant features and removing them in order to enhance the classifiers performance in terms of learning time and accuracy, and simplify the results to make them understandable. As shown previously, choosing a proper searching strategy in FS methods is very important to enhance the performance of the learning algorithm. By selecting the most informative feature and removing the irrelevant and redundant features, the dimensionality of the feature space will be reduced and the convergence speed of the learning algorithm will be improved [30]. In this regard, the SSA was selected to be utilized as an efficient optimization engine in a wrapper FS method since it has proven a satisfactory efficacy in tackling many optimization problems compared against other SI-based optimizers.

3.2. k-Nearest Neighbor Classifier (k-NN)

The k-NN algorithm is a simple non-parametric and instance-based classifier that relies on classifying unlabeled instances by measuring the distance between a given unlabeled instance and its closest k instances (k neighbors) [67]. The basic idea of this algorithm is that the label of some point in a given space is more likely to be similar to its closest points. There are different distance measurements utilized in the literature for k-NN. However, the most widely used measurement is the Euclidean distance which can be given as shown in Eq. 1.

$$dist(X_1 - X_2) = (\sum_{i=1}^{n}(x_{1i} - x_{2i})^2)^{0.5} \tag{1}$$

where X_1 and X_2 are two points with n dimensions.

3.3. Salp Swarm Algorithm

The main inspiration of SSA is the swarming behavior of sea organisms called salps. The salps are barrel-shaped, free floating tunicates from the family of Salpidae. Salps often float together in a form known as salp chain when navigating and foraging in oceans and seas as shown in Fig. 1. It is thought that a colony of salps move in this form for better locomotion and foraging.

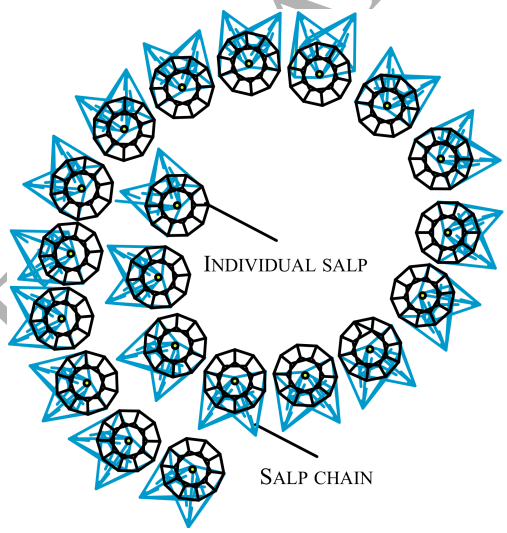


Figure 1: The demonstration of the salp chain

Similarly to other swarm intelligent algorithms, SSA is a population-based algorithm and starts by randomly initializing a predefined number of individuals. Each of these individuals represent a candidate solution for the targeted problem. There are two types of individuals in the swarm of the salps: a leader and followers. The leader is the first salp in the chain which guides the followers in their movement. A swarm X of n salps can be represented by a two-dimensional matrix as shown in Eq. 2. The target of this swarm is a food source in the search space called F.

$$X_i = \begin{bmatrix} x_1^1 & x_2^1 & \dots & x_d^1 \\ x_1^2 & x_2^2 & \dots & x_d^2 \\ \vdots & \vdots & \dots & \vdots \\ x_1^n & x_2^n & \dots & x_d^n \end{bmatrix} \tag{2}$$

The mathematical model that describes the salps chain is presented as follows. As mentioned before, the population is divided into two types of slaps, the leader and the followers. The leader position is updated using Eq. 3.

$$x_j^1 = \begin{cases} F_j + c_1 \left((ub_j - lb_j) \, c_2 + lb_j \right) & c_3 \geq 0.5 \\ F_j - c_1 \left((ub_j - lb_j) \, c_2 + lb_j \right) & c_3 < 0.5 \end{cases} \tag{3}$$

where x_j^1 and F_j are the positions of leaders and food source in the j^{th} dimension, respectively. c_1 is a variable that is gradually decreased over the course of iterations, and calculated as given in Eq. 4, where l and L are the current iteration and the maximum number of iterations, respectively. The other c_2 and c_3 variables in Eq. 3 are two numbers randomly drawn from the interval [0, 1]. The latter two variables are very important factors in SSA as they direct the next position in j^{th} dimension towards $+\infty$ or $-\infty$ as well as dictating the step size. The ub_j and lb_j are the upper and lower bounds of j^{th} dimension.

$$c_1 = 2e^{-(\frac{4l}{L})^2} \tag{4}$$

The positions of the followers salps are updated using Eq. 5.

$$x_j^i = \frac{1}{2}\left(x_j^i + x_j^{i-1}\right) \tag{5}$$

where $i \geq 2$ and x_j^i represents the position of the i^{th} follower at the j^{th} dimension.

The pseudocode of the basic SSA is presented in 1.

Algorithm 1 Pseudo-code of the SSA algorithm

```
Initialize the salp population x_i(i = 1, 2, ..., n) considering ub and lb
while (end condition is not satisfied) do
    Calculate the fitness of each search agent (salp)
    Set Fas the best search agent
    Update c_1 by Eq. 4
    for (each salp (x_i)) do
      if (i == 1) then
          Update the position of the leading salp by Eq. 3
      else
          Update the position of the follower salp by Eq. 5
    Update the salps based on the upper and lower bounds of variables
Return F
```

Like other SI algorithms, SSA starts the optimization process by generating a population of solutions (salps) randomly. Then, the generated solution is evaluated using an objective

function. In SSA, the fittest solution is denoted as the Food Source F which will be chased by other solutions (follower salps). At each iteration, c_1 variable is updated using Eq. 4, and each dimension in the leader (best salp) is updated using Eq. 3, while the positions of the followers salps are updated using Eq. 5. All the previous steps are repeated till a stopping criterion is satisfied. Since the solutions in population are very likely to be improved due to the exploration and exploitation processes, F should be updated during the optimization.

4. The Proposed Approaches

The SSA is a recent optimizer that has not been employed to tackle FS problems yet. It has many unique characteristics that make it favorable to be utilized as the searching engine in global optimization and FS problems. Initially, the SSA is efficient, flexible, simple and easy to implement. As a bonus, SSA has only one parameter to balance exploration and exploitation. This parameter is adaptively decreased over the course of iterations, which allows the SSA to explore most of the search space at the begging of the searching process and then exploit the promising areas at the final stages. Moreover, the positions of follower salps are updated gradually with respect to other members of the swarm, which helps the SSA to avoid trapping at local optima. Gradual movements of follower agents can avoid the SSA from effortlessly decaying in local solutions. The SSA retains the finest agent found so far and ascribes it to the food variable, consequently, it never get lost even if the entire agents get weaken. In the SSA, the leader salp moves based on the position of the food source only, which is the best salp attained so far, so the leader continually is capable of exploring and exploiting the space nearby the food source.

In the next section, two SSA approaches are proposed in a wrapper FS method. The first step is to prepare the SSA for tackling the FS by converting it to binary form since it is originally designed to deal with the continuous optimization problems. In the continuous SSA, salps can change their positions to any point in the search space, while in FS the movement is restricted to 0 and 1 values. Moreover, in the original SSA, the positions of the follower salps are updated by applying an average operator between a solution and its neighbor. In the second approaches, this average operator is replaced by a simple crossover operator which plays the same role in enhancing the exploratory behaviour of SSA.

4.1. Binary SSA (BSSA) with Transfer Functions

According to Mirjalili and Lewis [68], one of the most efficient ways to convert a continuous algorithm to a binary version is to utilize transfer functions (TF). In this work, eight TFs are used to convert the continuous SSA to binary version. These TFs belong to two different families, S-shaped and V-shaped. The purpose of a TF is to define a probability for updating an element in the feature subset (solution) to be 1 (selected) or 0 (not selected) as in Eq. 6, which was proposed by Kennedy and Eberhart [69] to covert the original PSO to a binary version.

$$T(x_j^i(t)) = \frac{1}{1 + \exp^{-x_j^i(t)}} \tag{6}$$

where x_j^i is the $j-th$ element in x solution in the $j-th$ dimension, and t is the current iteration.

Table 1: S-shaped and V-shaped transfer functions

S-shaped family		V-shaped family	
Name	Transfer function	Name	Transfer function
S1	$T(x) = \frac{1}{1+e^{-2x}}$	V1	$T(x) = \lvert\mathrm{erf}(\frac{\sqrt{\Pi}}{2}x)\rvert = \lvert\frac{\sqrt{2}}{\Pi}\int_0^{(\sqrt{\Pi}/2)x} e^{-t^2}dt\rvert$
S2	$T(x) = \frac{1}{1+e^{-x}}$	V2	$T(x) = \lvert\tanh(x)\rvert$
S3	$T(x) = \frac{1}{1+e^{(-x/2)}}$	V3	$T(x) = \lvert(x)/\sqrt{1+x^2}\rvert$
S4	$T(x) = \frac{1}{1+e^{(-x/3)}}$	V4	$T(x) = \lvert\frac{2}{\Pi}\mathrm{arc}\tan(\frac{\Pi}{2}x)\rvert$

In S-shaped family, an element of solution in the next iteration can be updated by Eq. 7

$$x_i^k(t+1) = \begin{cases} 0 & \text{If } rand < T(v_i^k(t+1)) \\ 1 & \text{If } rand \geq T(v_i^k(t+1)) \end{cases} \tag{7}$$

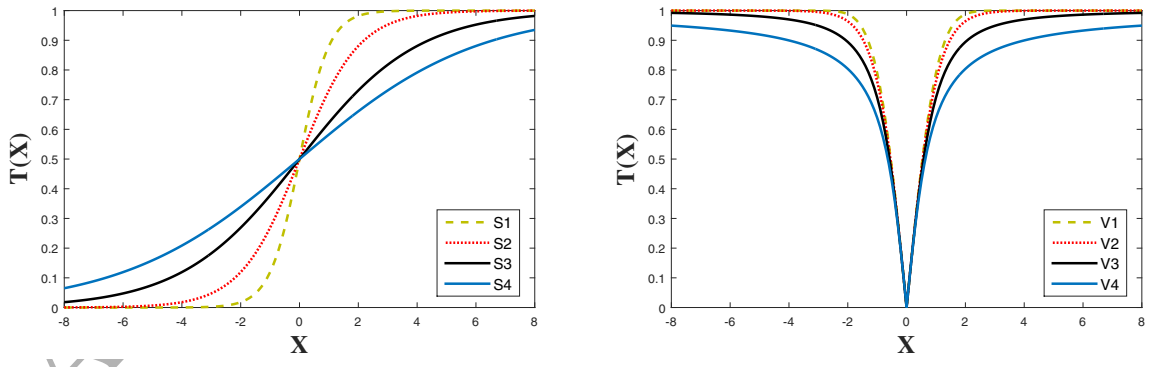
where $X_i^d(t+1)$ is the $i-th$ element at d^{th} dimension in X solution, $T(x_j^i(t))$ is the probability value, which can be obtained via Eq. 6.

In V-shaped family, an element of solution in the next iteration can be updated by Eq. 9, depending on the probability values obtained from Eq. 8, which was defined by Rashedi *et al.* [70] to covert the original GSA to a binary version.

$$T(x_j^i(t)) = \lvert\tanh(x_j^i(t))\rvert \tag{8}$$

$$X_{t+1} = \begin{cases} \neg X_t & r < T(\Delta x_{t+1}) \\ X_t & r \geq T(\Delta x_{t+1}) \end{cases} \tag{9}$$

Table 1 shows the mathematical formulation of all transfer functions used in this paper and Fig. 2 shows these two families of transfer functions.



(a) (b)

Figure 2: Transfer functions families (a) S-shaped and (b) V-shaped.

The flowchart of the the SSA algorithm with Transfer Functions is demonstrated in Fig. 3.

4.2. The BSSA with crossover scheme

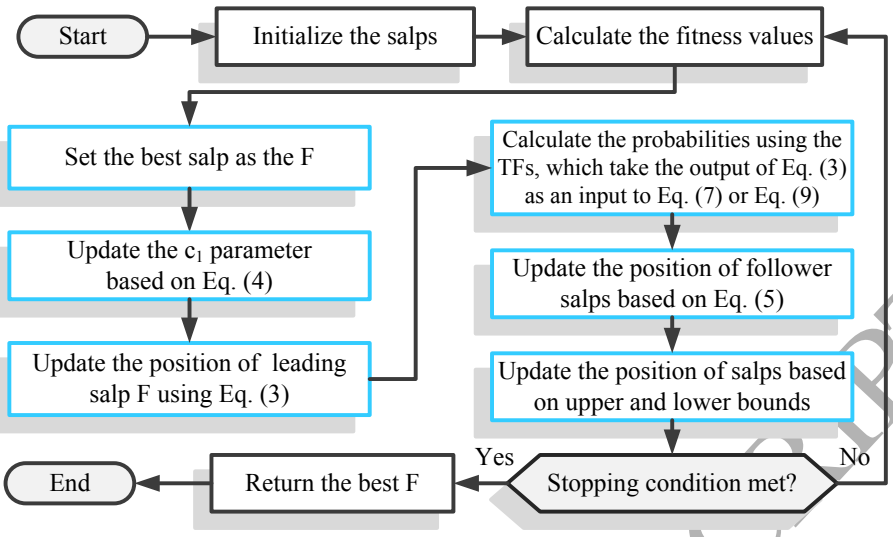


Figure 3: The flowchart of the SSA algorithm with Transfer Functions

In the proposed BSSA, the leader's position is updated by using a TF, while the followers' positions are updated using Eq. 5. This equation calculates a solution between two given solutions, which is helpful when the variables are continuous. This equation is useless for binary problems since there are only two values for the variables. To address this issue, we employ a crossover operator to combine solutions as shown in Eq. 10.

$$x_i^{t+1} = \bowtie (x_i, x_{i-1}) \tag{10}$$

where $\bowtie$ is an operator that performs the crossover scheme on two binary solutions, and x_i is the i^{th} follower salp. An example of this process can be seen in Fig. 4.

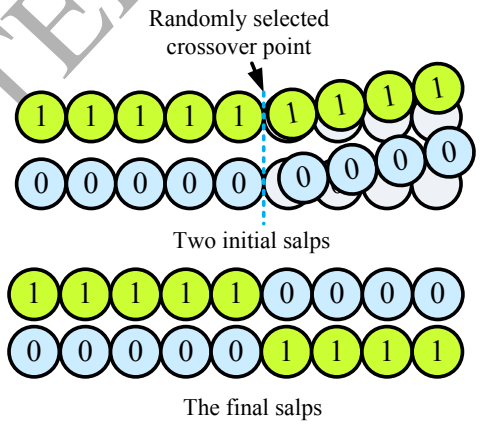


Figure 4: The crossover process

It can be seen in Fig. 4 that the binary bits are exchanged between two solutions, which causes abrupt changes in both solution. This is the main mechanism of global search and exploration in the proposed BSSA algorithm. Note that the crossover operator aims to obtain an intermediate solution in a binary search space to mimic the concept of finding a

solution between two solutions in Eq. 5. The crossover operator switches between two input vector with the same probability as given in Eq. 11.

$$x^d = \begin{cases} x_1^d & rand \geq 0.5 \\ x_2^d & otherwise \end{cases} \tag{11}$$

where x^d is the value of the d^{th} dimension in the resulted vector after applying the crossover operator on x_i and x_{i-1}.

The pseudocode of the proposed optimizer is presented in Algorithm 2

Algorithm 2 Pseudo-code of the SSA algorithm with Crossover operator

```
Initialize the salp population x_i(i = 1, 2, ..., n) considering ub and lb
while (end condition is not satisfied) do
    Calculate the fitness of each search agent (salp)
    Set F as the best search agent
    Update c_1 by Eq. 4
    for (each salp (x_i)) do
        if (i == 1) then
            Update the position of the leading salp by Eq. 3
            Calculate the probabilities using a TF which takes the output
            of Eq. 3 as its input (as in Eq. 7 (S-Shaped) or Eq. 9 (V-Shaped))
        else
            Update the position of the follower salp by performing a
            Crossover operator between x_i and x_{i-1} using Eq. 10.

    Update the salps based on the upper and lower bounds of variables
Return the best found solution F
```

5. Binary SSA for FS Problem

Two wrapper FS approaches that use SSA as a search algorithm and k-NN classifier as an evaluator were proposed. To formulate FS as an optimization problem, two key points should be taken into consideration; how to represent a solution and how to evaluate it. In this work, a feature subset is represented as a binary vector with a length equals to the number of features in the dataset. If a feature is set to 1, this means that it has been selected, otherwise it has not. The goodness of a feature subset is measured depending on two criteria; the maximum classification accuracy (minimum error rate) and simultaneously the minimal number of selected features. These two contradict objectives are represented in one fitness function that is shown in Eq. 12:

$$\downarrow Fitness = \alpha\gamma_R(D) + \beta\frac{|R|}{|C|} \tag{12}$$

where $\gamma_R(D)$ represents the classification error rate obtained by a specific classifier, |R| is the number of selected features in a reduct, and |C| is the number of conditional features in

the original dataset, and $\alpha \in [0,1]$, $\beta = (1-\alpha)$ are two parameters corresponding to the importance of classification quality and subset length as per recommendations in [41].

6. Experimental results and discussions

In this section, a comparative study is presented to carefully examine the exploratory and exploitative behavior of the proposed BSSA algorithms compared to several other well-established and novel metaheuristics. As case studies, 22 practical benchmark datasets are utilized. Table 2 describes these datasets in terms of number of features and number of instances. These datasets include several properties and cover various sizes and dimensions. For complete details about the origin and structure of these datasets, readers can refer to the sources available at UCI repository [71]. These problems can reveal the competency of the experienced optimizers in managing the exploration and exploitation trends and realizing more satisfactory results.

Table 2: List of used datasets

No.	Dataset	No. of Features	No. of instances
1.	Breastcancer	9	699
2.	BreastEW	30	596
3.	Exactly	13	1000
4.	Exactly2	13	1000
5.	HeartEW	13	270
6.	Lymphography	18	148
7.	M-of-n	13	1000
8.	PenglungEW	325	73
9.	SonarEW	60	208
10.	SpectEW	22	267
11.	CongressEW	16	435
12.	IonosphereEW	34	351
13.	KrvskpEW	36	3196
14.	Tic-tac-toe	9	958
15.	Vote	16	300
16.	WaveformEW	40	5000
17.	WineEW	13	178
18.	Zoo	16	101
19.	Clean1	166	476
20.	Semeion	265	1593
21.	Colon	2000	62
22.	Leukemia	7129	72

The developed variants of BSSA are implemented to discover the superior reduct in terms of error rate using KNN classifier with a Euclidean distance metric ($K = 5$ [41]). To validate the optimality of the results and substantiate the capabilities of algorithms, we use hold-out strategy where each dataset is randomly split into 80% for training and 20% for testing. To obtain statistically meaningful results, this split is repeated 30 independent times. Therefore, the statistical measurements are collected based on the overall capabilities and final results throughout 30 independent runs.The dimensions of the tackled problems are equal to number of features in the datasets.

All the tabulated evaluations and analyzed behaviors of the proposed BSSA are recorded and compared to other optimizers using a PC with Intel Core(TM) i5-5200U 2.2GHz CPU and 4.0GB RAM. All algorithms are tested using the MATLAB 2013 software. To have fair comparisons, all algorithms have been carefully implemented in the same programming language and by the same computing platform that can use the same global settings for all

algorithms. That is, all algorithms are uniformly randomly initialized. Moreover, for all algorithms the population size is set to 10 search agents, and the number of iterations is set to 100. These values are selected after conducting an initial empirical study by experimenting different values for the population size and number of iterations based on Leukemia dataset. This dataset was selected because it showed more sensitivity in comparison with other datasets. That is, significant changes in the performance of classifiers are noticed for slight changes in the parameter values [72]. As it can be seen in Table 3, a population size of 10 with 100 iterations managed to show very competitive results compared to larger population sizes and more iterations, which the latter require much more running time.

Table 3: Average accuracy results when using different combinations of population sizes and number of iterations based on Leukemia dataset.

Population size	10	50	100
Number of iterations	100	150	200
BSSA_S1	**0.9311**	0.8667	0.8667
BSSA_S2	0.9733	**1.0000**	**1.0000**
BSSA_S3	**1.0000**	0.9978	**1.0000**
BSSA_S4	**1.0000**	**1.0000**	**1.0000**
BSSA_V1	**1.0000**	**1.0000**	**1.0000**
BSSA_V2	**1.0000**	**1.0000**	**1.0000**
BSSA_V3	**1.0000**	0.9800	**1.0000**
BSSA_V4	0.9622	0.9378	**1.0000**

6.1. Assessment of the impact of α and β on the fitness function

The values of α and β in the fitness function reflect the weight of their corresponding terms for the user. That is, α determines the weight of the classification accuracy, while β corresponds to the weight of the features reduction rate. In majority of the previous works in literature, values of these parameters are set arbitrary. Traditionally, α is set to high value (i.e. $\alpha \geq 0.90$) and β is set to a very small value (i.e. $\beta \leq 0.5$). This experiment is conducted to study the influence of α and β on the performance of the basic BSSA with different TFs. The accuracy and the feature reduction rates are measured for different combinations of α and β values. These experiments are conducted based on Leukemia dataset because this dataset showed more sensitivity in comparison with other datasets. That is, significant changes in the performance of classifiers are noticed for slight changes in the parameter values [72]. The resulted accuracy rates are shown in Table 4, while the reduction rates are shown in Table 5. As it can be seen in the table, the accuracy rates are increased along with increasing the value of the α. On the other side, the impact of α and β on the feature reduction rate is shown in Table 5. In general, there is a decrease in the reduction rate by decreasing the value of β.

In order to make fair comparisons with the obtained results in previous works, we will set $\alpha = 0.99$ and $\beta = 0.01$ which are commonly used in the literature [41, 73].

6.2. Assessment of the proposed BSSA without crossover

In this subsection, the proposed BSSA-based algorithms are benchmarked on the 22 datasets to find the best version in dealing with FS problems. These binary versions utilize

Table 4: Impact of α and β on the accuracy rates based on Leukemia dataset.

α	**0.5**	**0.7**	**0.9**	**0.99**
β	**0.5**	**0.3**	**0.1**	**0.01**
Transfer Functions	AVE	AVE	AVE	AVE
BSSA_S1	0.8156	0.8578	0.8911	**0.9311**
BSSA_S2	0.9267	0.9578	0.9400	**0.9733**
BSSA_S3	0.9578	0.9778	**1.0000**	**1.0000**
BSSA_S4	0.8667	0.9333	0.9422	**1.0000**
BSSA_V1	0.8756	0.9422	0.9733	**1.0000**
BSSA_V2	0.8222	0.8867	0.9667	**1.0000**
BSSA_V3	0.9311	0.9689	0.9978	**1.0000**
BSSA_V4	0.9333	0.9578	0.9578	**0.9622**

Table 5: Impact of α and β on the feature reduction rate based on Leukemia dataset.

α	**0.5**	**0.7**	**0.9**	**0.99**
β	**0.5**	**0.3**	**0.1**	**0.01**
Transfer Functions	AVE	AVE	AVE	AVE
BSSA_S1	0.5066	0.4495	0.4706	0.3852
BSSA_S2	0.5019	0.4671	0.4979	0.4166
BSSA_S3	0.4510	0.4572	0.4707	0.5102
BSSA_S4	0.4733	0.5014	0.5002	0.5088
BSSA_V1	0.5042	0.4934	0.4501	0.4796
BSSA_V2	0.5041	0.5055	0.4309	0.5086
BSSA_V3	0.5028	0.4879	0.5063	0.5081
BSSA_V4	0.5038	0.4917	0.4824	0.4455

different S-shaped and V-shaped transfer functions, which were reported in Table 1. The efficacy of the BSSA-based versions are evaluated in using the average classification accuracy measure, selection size, average fitness, running time, and convergence behaviors on different problems. The accuracy is studied based on the selected features of the evaluated cases. The standard deviation (STD) of the versions in realizing the datasets is reported as well for all comparisons. To compare the effectiveness of multiple transfer functions in BSSA optimizer and detect significant improvements, the average ranking of the Friedman test is utilized here.

Table 6 shows the average fitness (AVE) and STD results for eight versions of BSSA.Tables 7-9 similarly demonstrate the accuracy results, average number of features, and running time records accompanied by the STD and ranking results of all versions of the BSSA optimizer. From Table 6, it is seen that the BSSA_S1 can provide the best fitness results on roughly 27% of the datasets. According to overall rankings, the best algorithm is the BSSA_V3, while the BSSA_S3, BSSA_S1, BSSA_S4, BSSA_V2, BSSA_S2, BSSA_V1, and BSSA_V4 are in the next stages.

Table 7 lists the results in terms of average accuracies. For the best and worst obtained accuracies we refer the reader to Table 25 in the appendix of tables. From Table 7, it can be seen that, in terms of classification accuracy, the BSSA with the first S-function outperforms all variants on around 27% of the datasets. The accuracy results of the binary version with V3 function are superior to those of other competitors according to overall rankings. According to the F-test results, those versions that utilize the S2, V1, and S4 transfer functions are in

Table 6: Comparison between different versions of BSSA (without crossover) based on S-shaped and V-shaped transfer functions in terms of average fitness results

Benchmark	Stat. Measure	BSSA_S1	BSSA_S2	BSSA_S3	BSSA_S4	BSSA_V1	BSSA_V2	BSSA_V3	BSSA_V4
Breastcancer	AVE	**0.0293**	0.0476	0.0308	0.0364	0.0393	0.0347	0.0377	0.0382
	STD	0.0000	0.0005	0.0015	0.0011	0.0022	0.0011	0.0017	0.0009
BreastEW	AVE	0.0583	0.0496	**0.0466**	0.0505	0.0528	0.0489	0.0487	0.0508
	STD	0.0041	0.0035	0.0044	0.0034	0.0040	0.0050	0.0057	0.0037
Exactly	AVE	**0.0121**	0.0162	0.0390	0.0211	0.0679	0.0740	0.0522	0.0771
	STD	0.0135	0.0171	0.0333	0.0229	0.0665	0.0630	0.0560	0.0626
Exactly2	AVE	0.2804	0.2649	0.2431	0.2379	0.2402	0.2748	**0.2336**	0.2538
	STD	0.0153	0.0089	0.0006	0.0056	0.0275	0.0125	0.0033	0.0233
HeartEW	AVE	**0.1572**	0.1780	0.1939	0.1641	0.1826	0.1939	0.1734	0.1769
	STD	0.0078	0.0116	0.0095	0.0105	0.0091	0.0103	0.0064	0.0100
Lymphography	AVE	**0.1326**	0.1924	0.1551	0.1585	0.1393	0.1557	0.1824	0.1923
	STD	0.0085	0.0109	0.0109	0.0128	0.0120	0.0150	0.0125	0.0146
M-of-n	AVE	0.0093	**0.0077**	0.0186	0.0167	0.0304	0.0299	0.0277	0.0213
	STD	0.0075	0.0050	0.0184	0.0119	0.0316	0.0319	0.0278	0.0209
PenglungEW	AVE	0.1592	0.1041	0.1882	0.1773	**0.0621**	0.1497	0.1048	0.1184
	STD	0.0117	0.0162	0.0141	0.0151	0.0093	0.0158	0.0115	0.0162
SonarEW	AVE	0.1403	0.1310	0.1159	0.1298	0.1044	**0.0679**	0.1126	0.1566
	STD	0.0097	0.0110	0.0136	0.0094	0.0104	0.0084	0.0117	0.0115
SpectEW	AVE	0.1896	0.1456	**0.1307**	0.1551	0.1707	0.1570	0.1550	0.1790
	STD	0.0077	0.0084	0.0090	0.0074	0.0052	0.0105	0.0090	0.0089
CongressEW	AVE	0.0463	0.0395	0.0437	0.0335	0.0482	**0.0249**	0.0416	0.0302
	STD	0.0050	0.0046	0.0050	0.0036	0.0039	0.0053	0.0042	0.0044
IonosphereEW	AVE	0.1027	0.0807	0.0786	0.1139	0.0704	0.0728	**0.0550**	0.1006
	STD	0.0054	0.0049	0.0067	0.0074	0.0074	0.0114	0.0053	0.0083
KrvskpEW	AVE	0.0439	**0.0348**	0.0487	0.0450	0.0523	0.0518	0.0567	0.0500
	STD	0.0048	0.0040	0.0038	0.0056	0.0081	0.0071	0.0067	0.0073
Tic-tac-toe	AVE	0.2175	0.2120	**0.1972**	0.2247	0.1998	0.2154	0.2091	0.2114
	STD	0.0000	0.0026	0.0041	0.0034	0.0063	0.0023	0.0029	0.0076
Vote	AVE	0.0471	0.0541	0.0456	**0.0337**	0.0709	0.0597	0.0542	0.0493
	STD	0.0058	0.0054	0.0035	0.0060	0.0052	0.0046	0.0036	0.0078
WaveformEW	AVE	**0.2671**	0.2722	0.2703	0.2718	0.2773	0.2734	0.2838	0.2751
	STD	0.0039	0.0057	0.0066	0.0052	0.0068	0.0081	0.0073	0.0071
WineEW	AVE	**0.0140**	0.0412	0.0354	0.0256	0.0253	0.0279	0.0190	0.0288
	STD	0.0049	0.0048	0.0044	0.0035	0.0069	0.0054	0.0087	0.0065
Zoo	AVE	0.0704	0.0446	**0.0047**	0.0609	0.0486	0.0440	0.0427	0.0438
	STD	0.0092	0.0005	0.0005	0.0064	0.0080	0.0006	0.0117	0.0009
Clean1	AVE	0.1592	0.1083	0.1100	**0.1048**	0.1327	0.1240	0.1080	0.1224
	STD	0.0053	0.0049	0.0059	0.0059	0.0049	0.0073	0.0056	0.0081
Semeion	AVE	0.0286	0.0299	0.0289	0.0369	0.0274	0.0304	**0.0246**	0.0259
	STD	0.0014	0.0017	0.0012	0.0018	0.0016	0.0018	0.0018	0.0018
Colon	AVE	0.1635	0.2630	0.2184	0.2894	0.2463	0.1670	0.2037	**0.1570**
	STD	0.0058	0.0079	0.0152	0.0097	0.0242	0.0379	0.0248	0.0216
Leukemia	AVE	0.0743	0.0322	**0.0049**	**0.0049**	0.0052	**0.0049**	**0.0049**	0.0429
	STD	0.0118	0.0326	0.0000	0.0000	0.0006	0.0000	0.0000	0.0326
Ranking	**W|T|L**	**6|0|16**	2|0|22	4|1|17	2|1|19	1|0|21	2|1|19	3|1|18	1|0|21
Overall Ranking	**F-Test**	4.4091	4.7727	3.9318	4.5455	4.9091	4.75	**3.7273**	4.9545

Table 7: Comparison between different versions of BSSA (without crossover) based on S-shaped and V-shaped transfer functions in terms of average accuracy.

Benchmark	Stat. Measure	BSSA_S1	BSSA_S2	BSSA_S3	BSSA_S4	BSSA_V1	BSSA_V2	BSSA_V3	BSSA_V4
Breastcancer	AVE	**0.9771**	0.9571	0.9743	0.9686	0.9659	0.9707	0.9678	0.9684
	STD	0.0000	0.0000	0.0000	0.0000	0.0025	0.0018	0.0018	0.0007
BreastEW	AVE	0.9478	0.9557	**0.9584**	0.9544	0.9516	0.9551	0.9554	0.9528
	STD	0.0041	0.0036	0.0046	0.0033	0.0042	0.0046	0.0053	0.0038
Exactly	AVE	**0.9932**	0.9891	0.9663	0.9843	0.9374	0.9313	0.9533	0.9281
	STD	0.0132	0.0169	0.0332	0.0227	0.0665	0.0629	0.0558	0.0625
Exactly2	AVE	0.7239	0.7392	0.7560	0.7611	0.7589	0.7277	**0.7655**	0.7467
	STD	0.0134	0.0087	0.0000	0.0047	0.0270	0.0119	0.0029	0.0212
HeartEW	AVE	**0.8467**	0.8257	0.8104	0.8395	0.8217	0.8089	0.8299	0.8272
	STD	0.0071	0.0113	0.0096	0.0107	0.0101	0.0104	0.0071	0.0109
Lymphography	AVE	**0.8734**	0.8113	0.8491	0.8455	0.8644	0.8473	0.8203	0.8099
	STD	0.0090	0.0109	0.0113	0.0131	0.0125	0.0155	0.0129	0.0154
M-of-n	AVE	0.9960	**0.9977**	0.9869	0.9887	0.9753	0.9758	0.9777	0.9843
	STD	0.0072	0.0047	0.0181	0.0116	0.0315	0.0315	0.0274	0.0205
PenglungEW	AVE	0.8450	0.9009	0.8153	0.8261	**0.9414**	0.8523	0.8973	0.8838
	STD	0.0122	0.0164	0.0143	0.0154	0.0102	0.0154	0.0110	0.0161
SonarEW	AVE	0.8654	0.8744	0.8885	0.8740	0.8997	**0.9365**	0.8910	0.8465
	STD	0.0098	0.0113	0.0137	0.0096	0.0106	0.0086	0.0119	0.0117
SpectEW	AVE	0.8139	0.8585	**0.8741**	0.8483	0.8306	0.8465	0.8478	0.8239
	STD	0.0078	0.0084	0.0091	0.0072	0.0056	0.0109	0.0091	0.0093
CongressEW	AVE	0.9584	0.9645	0.9593	0.9699	0.9535	**0.9795**	0.9624	0.9723
	STD	0.0050	0.0047	0.0051	0.0035	0.0036	0.0056	0.0042	0.0044
IonosphereEW	AVE	0.9028	0.9241	0.9258	0.8892	0.9331	0.9305	**0.9487**	0.9021
	STD	0.0055	0.0048	0.0068	0.0076	0.0074	0.0110	0.0053	0.0081
KrvskpEW	AVE	0.9629	**0.9711**	0.9570	0.9606	0.9523	0.9529	0.9479	0.9546
	STD	0.0048	0.0037	0.0036	0.0055	0.0086	0.0072	0.0068	0.0074
Tic-tac-toe	AVE	0.7871	0.7926	**0.8086**	0.7789	0.8052	0.7895	0.7947	0.7933
	STD	0.0000	0.0026	0.0045	0.0029	0.0074	0.0020	0.0027	0.0076
Vote	AVE	0.9571	0.9491	0.9584	**0.9696**	0.9324	0.9433	0.9500	0.9536
	STD	0.0057	0.0057	0.0042	0.0060	0.0057	0.0045	0.0042	0.0075
WaveformEW	AVE	**0.7379**	0.7315	0.7328	0.7316	0.7255	0.7291	0.7190	0.7271
	STD	0.0039	0.0056	0.0067	0.0052	0.0068	0.0077	0.0072	0.0071
WineEW	AVE	**0.9918**	0.9633	0.9704	0.9794	0.9794	0.9768	0.9858	0.9753
	STD	0.0051	0.0051	0.0055	0.0043	0.0073	0.0051	0.0093	0.0069
Zoo	AVE	0.9340	0.9608	**1.0000**	0.9438	0.9562	0.9608	0.9621	0.9608
	STD	0.0096	0.0000	0.0000	0.0068	0.0084	0.0000	0.0114	0.0000
Clean1	AVE	0.8462	0.8969	0.8945	**0.8996**	0.8706	0.8793	0.8955	0.8805
	STD	0.0057	0.0050	0.0060	0.0060	0.0050	0.0071	0.0055	0.0079
Semeion	AVE	0.9783	0.9762	0.9764	0.9681	0.9774	0.9742	**0.9801**	0.9789
	STD	0.0014	0.0018	0.0012	0.0018	0.0017	0.0019	0.0019	0.0017
Colon	AVE	0.8398	0.7398	0.7849	0.7129	0.7538	0.8344	0.7978	**0.8441**
	STD	0.0059	0.0082	0.0155	0.0098	0.0232	0.0367	0.0239	0.0209
Leukemia	AVE	0.9311	0.9733	**1.0000**	**1.0000**	**1.0000**	**1.0000**	**1.0000**	0.9622
	STD	0.0122	0.0332	0.0000	0.0000	0.0000	0.0000	0.0000	0.0336
Ranking	**W|T|L**	**6|0|16**	2|0|20	4|1|17	2|1|19	2|1|19	2|1|19	3|1|18	1|0|21
Overall Ranking	**F-Test**	4.3182	4.5455	3.9091	4.5	4.9773	4.8182	**3.8636**	5.0682

the next places.

Table 8: Comparison between different versions of BSSA (without crossover) based on S-shaped and V-shaped transfer functions in terms of average number of features

Benchmark	Stat. Measure	BSSA_S1	BSSA_S2	BSSA_S3	BSSA_S4	BSSA_V1	BSSA_V2	BSSA_V3	BSSA_V4
Breastcancer	AVE	6.0000	**4.6333**	4.8000	4.7333	5.0000	5.0667	5.2333	6.2333
	STD	0.0000	0.4901	1.3493	0.9803	0.7428	0.9072	0.5040	0.4302
BreastEW	AVE	19.8333	17.2000	16.0000	16.0667	14.5333	13.4333	13.8333	**11.9333**
	STD	2.1669	2.5380	2.3342	2.6121	2.8129	3.4309	3.6111	3.2898
Exactly	AVE	**6.9667**	7.0000	7.4000	7.2000	7.7000	7.8667	7.7000	7.7333
	STD	0.6687	0.6433	0.7701	0.6644	1.0222	0.9371	1.0875	1.0483
Exactly2	AVE	9.2000	8.7333	2.0333	**1.8000**	1.9000	6.7667	1.8667	3.8667
	STD	2.7342	0.7397	0.7649	1.2972	1.0619	2.4591	0.8996	3.3501
HeartEW	AVE	6.9667	7.0000	8.0333	6.8333	7.9333	**6.1000**	6.4667	7.5000
	STD	1.6291	1.4622	1.2726	1.2058	1.8182	1.5166	1.7564	1.4081
Lymphography	AVE	13.1333	9.9000	10.2333	9.9667	9.1667	8.1333	8.1000	**7.3333**
	STD	1.1366	1.3734	1.7357	1.5196	2.8416	3.0820	2.9167	2.1227
M-of-n	AVE	**6.9333**	7.0333	7.2667	7.2000	7.7333	7.7333	7.3333	7.4333
	STD	0.6915	0.5561	0.6397	0.7144	0.8683	1.0148	1.0283	0.9353
PenglungEW	AVE	189.5000	195.4333	172.7333	167.7000	133.8667	111.0333	**103.1333**	109.1667
	STD	25.5920	10.7405	9.1234	7.9791	40.3431	54.1113	55.9715	50.0221
SonarEW	AVE	42.2667	39.8667	32.7333	30.7667	30.3667	30.6667	28.1667	**27.6333**
	STD	3.0954	4.4313	2.6253	3.3081	3.2641	4.3417	4.2757	4.7524
SpectEW	AVE	11.8000	12.0000	13.3000	10.6333	**6.5000**	11.1667	9.3333	10.2667
	STD	2.1877	2.3342	2.0703	2.3413	3.6742	2.2907	2.5371	2.0331
CongressEW	AVE	8.1333	7.0333	5.4333	5.9333	**3.5333**	7.3333	6.9000	4.4667
	STD	1.2521	2.2047	1.4547	1.4840	2.2854	1.9885	1.6474	1.9954
IonosphereEW	AVE	22.0333	18.9000	17.2667	14.3667	14.2667	13.7000	14.2667	**12.5000**
	STD	3.5862	2.3831	3.0731	2.3706	2.7535	3.5926	3.3107	3.5307
KrvskpEW	AVE	25.6667	22.2667	21.9000	21.6000	**18.2000**	18.4667	18.3000	**18.2000**
	STD	2.1549	2.1324	2.3976	2.4719	4.4443	3.0141	3.4356	3.4978
Tic-tac-toe	AVE	6.0000	6.0000	6.9000	**5.2667**	6.2333	6.3000	**5.2667**	6.0667
	STD	0.0000	0.0000	0.3051	0.6915	0.8584	0.9154	0.5208	0.3651
Vote	AVE	7.4667	5.9667	7.1333	5.7667	6.3667	5.7000	7.4667	**5.3333**
	STD	1.2521	1.5862	2.1772	1.8696	2.0592	2.4233	2.7759	2.0734
WaveformEW	AVE	30.4333	25.4000	23.3333	24.0667	22.0667	20.7000	22.4333	**19.6333**
	STD	2.0457	2.8357	2.6305	2.7409	3.7318	4.1369	4.1163	3.2322
WineEW	AVE	7.6333	6.3667	7.9667	6.8333	6.4333	6.3667	6.4000	**5.6333**
	STD	0.8087	1.1592	2.0924	1.3917	1.6333	1.8286	1.5669	1.0662
Zoo	AVE	8.1333	9.2667	**7.5667**	8.3333	8.4333	8.2667	8.2000	7.9667
	STD	0.8996	0.7849	0.7739	1.0613	1.4308	0.9444	1.4239	1.3767
Clean1	AVE	115.5667	103.5667	93.2333	89.5000	76.7000	75.1000	75.5000	**68.9667**
	STD	13.1193	7.4772	8.7678	5.6614	13.0758	14.8982	16.6604	16.7507
Semeion	AVE	190.0333	166.2333	148.1333	140.8000	134.4000	**129.4667**	131.4000	132.2333
	STD	23.1181	8.0288	7.3940	9.7994	7.7797	17.6728	7.3700	13.6904
Colon	AVE	984.9000	1079.4333	1093.0000	1044.6667	**502.8333**	608.8000	710.2333	533.2333
	STD	17.4224	105.4853	36.7283	31.5391	426.8525	418.4239	393.4634	381.6319
Leukemia	AVE	4382.8000	4159.2670	**3491.8670**	3501.6670	3709.9670	3503.2670	3506.8670	3953.0670
	STD	415.7237	346.0309	31.9145	23.3036	398.4409	25.7266	25.2870	632.9743
Ranking	W|T|L	2|0|20	1|0|21	1|0|21	2|0|20	4|0|18	2|0|20	2|0|20	9|0|13
Overall Ranking	F-Test	6.3182	5.6818	5.5909	4.3864	3.9545	3.7727	3.3636	**2.9318**

Inspecting the results in Table 8, it can be spotted that the proposed BSSA with V4 transfer function provides the lower number of features than others in around 41% of the datasets with the best ranking. Regarding the ranks, the BSSA with V-shaped transfer functions can provide better results than those with S-shaped functions.

From Table 9, it is evident that the V4 can decrease the running time of the algorithm more than other choices. The transfer functions V2, V3, V1, S4, S3, S1, and S2 can be the next choices, respectively.

6.3. Assessment of the proposed BSSA with crossover

In this section we assess the performance of BSSA combined with crossover and compare its performance to the basic BSSA that has no crossover operator.

Table 10 reveals the average fitness results of the BSSA with S-shaped TFs and the proposed BSSA with crossover operator and S-shaped TFs. From this table, it is seen

Table 9: Comparison between different versions of BSSA (without crossover) based on S-shaped and V-shaped transfer functions in terms of average running time

Benchmark	Stat. Measure	BSSA_S1	BSSA_S2	BSSA_S3	BSSA_S4	BSSA_V1	BSSA_V2	BSSA_V3	BSSA_V4
Breastcancer	AVE	6.3419	6.1287	6.0900	6.0691	6.0650	6.0793	**6.0087**	6.0535
	STD	0.2242	0.1176	0.1593	0.1416	0.1542	0.1310	0.1391	0.1472
BreastEW	AVE	6.9568	6.8192	6.7886	6.7479	6.7490	6.7242	6.7241	**6.7204**
	STD	0.1544	0.1412	0.1368	0.1365	0.1548	0.1054	0.1468	0.1474
Exactly	AVE	9.1079	8.8297	8.7315	8.5636	8.4290	8.3918	**8.3905**	8.4522
	STD	0.1820	0.1895	0.1461	0.1479	0.1691	0.1605	0.1509	0.1756
Exactly2	AVE	9.2486	8.9892	8.6881	8.6479	8.5800	8.5698	8.6158	**8.5339**
	STD	0.2807	0.1765	0.1530	0.1408	0.2083	0.1446	0.1493	0.1533
HeartEW	AVE	4.8109	4.7856	4.8080	4.7876	4.7885	4.7795	4.8058	**4.7629**
	STD	0.1153	0.1266	0.1547	0.1490	0.1485	0.1241	0.1435	0.1143
Lymphography	AVE	**4.5691**	4.6016	4.5918	4.5776	4.5928	4.5818	4.5852	4.5817
	STD	0.1373	0.1310	0.1321	0.1051	0.1266	0.1128	0.1135	0.1230
M-of-n	AVE	8.9426	8.7137	8.5289	8.4811	8.4435	8.3370	8.3191	**8.2535**
	STD	0.1567	0.1353	0.1652	0.1800	0.1867	0.1428	0.1603	0.1564
PenglungEW	AVE	6.9319	7.0017	6.9723	6.9908	7.0545	6.8316	6.7966	**6.7937**
	STD	0.1779	0.2111	0.1598	0.1647	0.2331	0.1739	0.1856	0.1474
SonarEW	AVE	5.2936	5.2877	5.2625	5.2572	5.2337	5.1985	**5.1945**	5.2115
	STD	0.1417	0.1429	0.1502	0.1306	0.1504	0.1372	0.1408	0.1676
SpectEW	AVE	4.8724	4.8749	4.9058	**4.8595**	4.8817	4.8618	4.8952	4.8630
	STD	0.1254	0.1179	0.1166	0.0954	0.1349	0.1129	0.0963	0.1024
CongressEW	AVE	5.4705	5.4873	5.4636	5.4580	5.4406	5.4539	**5.4404**	5.4507
	STD	0.1292	0.0989	0.0971	0.1208	0.1466	0.1434	0.1103	0.1372
IonosphereEW	AVE	5.5331	5.5000	5.4766	5.4798	5.5120	5.4691	5.4667	**5.4471**
	STD	0.1344	0.1397	0.1002	0.1013	0.1217	0.1286	0.1224	0.1224
KrvskpEW	AVE	90.1701	85.5203	83.3227	82.4860	80.9167	80.8368	80.9479	**80.7104**
	STD	1.0019	0.6986	0.7765	0.7200	0.7489	0.9229	0.8432	0.8994
Tic-tac-toe	AVE	8.3671	8.6742	8.4558	8.4044	8.3256	**8.2557**	8.3069	8.2683
	STD	0.1682	0.1747	0.1625	0.1808	0.1533	0.1268	0.1958	0.1660
Vote	AVE	4.9164	4.9204	4.8939	4.9023	4.8986	4.8907	4.8872	**4.8821**
	STD	0.1268	0.1445	0.1002	0.1203	0.1053	0.1177	0.1121	0.1202
WaveformEW	AVE	233.4317	219.4103	211.4342	209.5122	203.5272	**203.0986**	203.7187	203.3405
	STD	2.6403	2.4184	1.5368	1.6556	2.0957	1.9709	2.3329	2.0857
WineEW	AVE	4.5797	4.5874	4.5819	4.5683	4.5612	**4.5252**	4.5425	4.5563
	STD	0.1356	0.1068	0.1281	0.1213	0.1273	0.0992	0.1021	0.1120
Zoo	AVE	4.5614	4.5935	4.5761	4.5770	4.5990	4.5575	4.5501	**4.5438**
	STD	0.1179	0.1361	0.1149	0.1313	0.1089	0.1098	0.1355	0.1457
Clean1	AVE	14.5884	14.0300	13.6366	13.5364	13.2981	13.1682	13.2241	**13.1324**
	STD	0.3487	0.3311	0.3186	0.3236	0.3548	0.3357	0.3146	0.3455
Semeion	AVE	171.5068	160.8404	152.9361	150.4326	145.3891	145.4128	145.8595	**145.3749**
	STD	2.6292	1.4173	1.2590	1.1394	1.8617	1.7401	1.5058	1.5577
Colon	AVE	18.7257	19.0884	19.2046	19.2324	19.3587	18.1871	18.1081	**18.0409**
	STD	0.5844	0.5838	0.6449	0.6399	0.9240	0.5712	0.5278	0.5719
Leukemia	AVE	29.0596	26.0303	**24.4623**	24.5787	26.8454	26.4626	28.1687	27.0976
	STD	2.3031	2.4104	1.2403	1.1275	1.3364	0.8502	2.0315	1.3519
Ranking	**W|T|L**	1|0|21	0|0|22	1|0|21	1|0|21	0|0|22	3|0|19	4|0|18	12|0|10
Overall Ranking	**F-Test**	6.6364	6.8182	5.9091	4.8636	4.6364	2.5909	2.8182	1.7273

that the BSSA_S3_CP and BSSA_S2_CP can significantly outperform the BSSA_S3 and BSSA_S3 on 73% of the datasets, respectively. The BSSA_S2_CP can disclose superior results compared to the BSSA_S2 in 54% of the datasets. The BSSA_S4_CP outperforms the BSSA_S4 on 68% problems. The reason is that the embedded crossover operator has enhanced the exploration capacity of BSSA_S3_CP and BSSA_S2_CP compared to those versions that utilize the standard average operator. Hence, in the case of premature convergence the BSSA-based methods with crossover theme have more chance to escape from them by more iteration and then, smoothly, switch from broad exploration to focused exploitation around the food source. Based on the overall ranks at the end of Table 10, the BSSA_S3_CP have attained the best rank among other competitors in terms of the average fitness values.

Table 10: Comparison between the BSSA with S-shaped functions (without crossover) and the proposed BSSA combined with CP in terms of average fitness results.

Benchmark	Stat. Measure	BSSA_S1	BSSA_S1_CP	BSSA_S2	BSSA_S2_CP	BSSA_S3	BSSA_S3_CP	BSSA_S4	BSSA_S4_CP
Breastcancer	AVE	**0.0293**	0.0447	0.0476	**0.0312**	0.0308	**0.0273**	0.0364	**0.0227**
	STD	0.0000	0.0019	0.0005	0.0032	0.0015	0.0006	0.0011	0.0005
BreastEW	AVE	0.0583	**0.0448**	**0.0496**	0.0551	**0.0466**	0.0566	0.0505	**0.0442**
	STD	0.0041	0.0035	0.0035	0.0056	0.0044	0.0033	0.0034	0.0030
Exactly	AVE	**0.0121**	0.0146	0.0162	**0.0088**	0.0390	**0.0251**	**0.0211**	0.0231
	STD	0.0135	0.0127	0.0171	0.0047	0.0333	0.0254	0.0229	0.0211
Exactly2	AVE	0.2804	**0.2561**	0.2649	**0.2512**	0.2431	**0.2415**	**0.2379**	0.2818
	STD	0.0153	0.0081	0.0089	0.0107	0.0006	0.0197	0.0056	0.0073
HeartEW	AVE	**0.1572**	0.1711	0.1780	**0.1691**	0.1939	**0.1426**	0.1641	**0.1604**
	STD	0.0078	0.0053	0.0116	0.0075	0.0095	0.0074	0.0105	0.0077
Lymphography	AVE	**0.1326**	0.1674	0.1924	**0.1630**	0.1551	**0.1146**	0.1585	**0.1332**
	STD	0.0085	0.0092	0.0109	0.0118	0.0109	0.0108	0.0128	0.0085
M-of-n	AVE	0.0093	**0.0076**	0.0077	**0.0064**	0.0186	**0.0136**	0.0167	**0.0115**
	STD	0.0075	0.0068	0.0050	0.0043	0.0184	0.0136	0.0119	0.0079
PenglungEW	AVE	0.1592	**0.0853**	**0.1041**	0.2147	0.1882	**0.1266**	0.1773	**0.0816**
	STD	0.0117	0.0084	0.0162	0.0098	0.0141	0.0134	0.0151	0.0091
SonarEW	AVE	0.1403	**0.0776**	0.1310	**0.1100**	0.1159	**0.0678**	0.1298	**0.1131**
	STD	0.0097	0.0076	0.0110	0.0105	0.0136	0.0095	0.0094	0.0098
SpectEW	AVE	0.1896	**0.1479**	**0.1456**	0.1632	**0.1307**	0.1673	**0.1551**	0.1678
	STD	0.0077	0.0050	0.0084	0.0067	0.0090	0.0044	0.0074	0.0082
CongressEW	AVE	0.0463	**0.0375**	0.0395	**0.0345**	0.0437	**0.0404**	**0.0335**	0.0386
	STD	0.0050	0.0056	0.0046	0.0033	0.0050	0.0037	0.0036	0.0052
IonosphereEW	AVE	**0.1027**	0.1413	0.0807	**0.0762**	**0.0786**	0.0857	0.1139	**0.1000**
	STD	0.0054	0.0059	0.0049	0.0048	0.0067	0.0080	0.0074	0.0059
KrvskpEW	AVE	0.0439	**0.0411**	**0.0348**	0.0397	0.0487	**0.0410**	0.0450	**0.0446**
	STD	0.0048	0.0037	0.0040	0.0047	0.0038	0.0058	0.0056	0.0068
Tic-tac-toe	AVE	0.2175	**0.2135**	**0.2120**	0.2222	0.1972	**0.1844**	0.2247	**0.2098**
	STD	0.0000	0.0069	0.0026	0.0028	0.0041	0.0000	0.0034	0.0038
Vote	AVE	0.0471	**0.0420**	0.0541	**0.0523**	**0.0456**	0.0514	**0.0337**	0.0549
	STD	0.0058	0.0093	0.0054	0.0032	0.0035	0.0057	0.0060	0.0042
WaveformEW	AVE	**0.2671**	0.2709	0.2722	**0.2658**	0.2703	**0.2695**	0.2718	**0.2711**
	STD	0.0039	0.0047	0.0057	0.0061	0.0066	0.0071	0.0052	0.0072
WineEW	AVE	0.0140	**0.0077**	0.0412	**0.0279**	0.0354	**0.0115**	**0.0256**	0.0350
	STD	0.0049	0.0035	0.0048	0.0021	0.0044	0.0057	0.0035	0.0043
Zoo	AVE	**0.0704**	0.1015	0.0446	**0.0438**	0.0047	**0.0042**	0.0609	**0.0401**
	STD	0.0092	0.0155	0.0005	0.0005	0.0005	0.0004	0.0064	0.0064
Clean1	AVE	0.1592	**0.1168**	0.1083	**0.1051**	**0.1100**	0.1248	**0.1048**	0.1079
	STD	0.0053	0.0068	0.0049	0.0048	0.0059	0.0041	0.0059	0.0067
Semeion	AVE	**0.0286**	0.0322	**0.0299**	0.0338	0.0289	**0.0255**	0.0369	**0.0308**
	STD	0.0014	0.0017	0.0017	0.0016	0.0012	0.0014	0.0018	0.0015
Colon	AVE	**0.1635**	0.2464	0.2630	**0.1390**	**0.2184**	0.3163	0.2894	**0.1255**
	STD	0.0058	0.0156	0.0079	0.0119	0.0152	0.0185	0.0097	0.0137
Leukemia	AVE	0.0743	**0.0123**	0.0322	**0.0051**	**0.0049**	0.0166	**0.0049**	0.0765
	STD	0.0118	0.0199	0.0326	0.0003	0.0000	0.0247	0.0000	0.0165
Ranking	W|T|L	9|0|13	13|0|9	6|0|16	**16|0|6**	7|0|15	**15|0|7**	8|0|14	14|0|8
Overall Ranking	F-Test	4.8636	4.2727	5.2273	3.8182	4.7727	**3.6818**	5.0909	4.2727

In Table 11 we list the fitness results of the proposed BSSA methods with V-shaped TFs.According to this table, it is observed that the BSSA_V2_CP can obtain significantly

better fitness measures than the BSSA_V2 on 59% of the datasets. The crossover operator has also improved the fitness values of BSSA_V4 algorithm on 12 cases. The reason is that the crossover operator improves the exploratory characteristic of the BSSA_V2 and BSSA_V4 variants. As such, it can jump out of sub-optimal solutions more efficiently, whereas the other competitors are still disposed to stagnation to local solutions. Based on the overall ranks, the BSSA with V2 and CP has demonstrated a better efficacy than other techniques.

Table 11: Comparison between the BSSA with V-shaped functions and the proposed BSSA with CP regarding the average fitness results.

Benchmark	Stat. Measure	BSSA_V1	BSSA_V1_CP	BSSA_V2	BSSA_V2_CP	BSSA_V3	BSSA_V3_CP	BSSA_V4	BSSA_V4_CP
Breastcancer	AVE	0.0393	**0.0331**	0.0347	**0.0278**	0.0377	**0.0324**	0.0382	**0.0371**
	STD	0.0022	0.0007	0.0011	0.0016	0.0017	0.0005	0.0009	0.0029
BreastEW	AVE	0.0528	**0.0435**	0.0489	**0.0385**	**0.0487**	0.0640	0.0508	**0.0445**
	STD	0.0040	0.0042	0.0050	0.0041	0.0057	0.0049	0.0037	0.0039
Exactly	AVE	0.0679	**0.0390**	0.0740	**0.0467**	0.0522	**0.0413**	0.0771	**0.0294**
	STD	0.0665	0.0446	0.0630	0.0527	0.0560	0.0370	0.0626	0.0286
Exactly2	AVE	**0.2402**	0.2639	0.2748	**0.2448**	**0.2336**	0.2838	**0.2538**	0.2727
	STD	0.0275	0.0127	0.0125	0.0005	0.0033	0.0089	0.0233	0.0120
HeartEW	AVE	0.1826	**0.1767**	0.1939	**0.1714**	**0.1734**	0.1779	**0.1769**	0.1820
	STD	0.0091	0.0104	0.0103	0.0080	0.0064	0.0099	0.0100	0.0101
Lymphography	AVE	**0.1393**	0.1581	0.1557	**0.1382**	**0.1824**	0.1958	0.1923	**0.1520**
	STD	0.0120	0.0142	0.0150	0.0149	0.0125	0.0109	0.0146	0.0169
M-of-n	AVE	0.0304	**0.0163**	0.0299	**0.0192**	**0.0277**	0.0318	**0.0213**	0.0243
	STD	0.0316	0.0146	0.0319	0.0236	0.0278	0.0370	0.0209	0.0235
PenglungEW	AVE	**0.0621**	0.1752	0.1497	**0.0844**	**0.1048**	0.1183	**0.1184**	0.1237
	STD	0.0093	0.0185	0.0158	0.0008	0.0115	0.0174	0.0162	0.0135
SonarEW	AVE	**0.1044**	0.1139	**0.0679**	0.1014	0.1126	**0.1021**	0.1566	**0.1062**
	STD	0.0104	0.0125	0.0084	0.0075	0.0117	0.0105	0.0115	0.0110
SpectEW	AVE	**0.1707**	0.1948	**0.1570**	0.1771	0.1550	**0.1337**	0.1790	**0.1693**
	STD	0.0052	0.0131	0.0105	0.0096	0.0090	0.0061	0.0089	0.0116
CongressEW	AVE	0.0482	**0.0317**	**0.0249**	0.0438	**0.0416**	0.0456	**0.0302**	0.0306
	STD	0.0039	0.0036	0.0053	0.0061	0.0042	0.0058	0.0044	0.0095
IonosphereEW	AVE	**0.0704**	0.0924	**0.0728**	0.1089	**0.0550**	0.0886	0.1006	**0.0949**
	STD	0.0074	0.0066	0.0114	0.0100	0.0053	0.0089	0.0083	0.0076
KrvskpEW	AVE	0.0523	**0.0508**	**0.0518**	0.0604	0.0567	**0.0512**	**0.0500**	0.0521
	STD	0.0081	0.0095	0.0071	0.0069	0.0067	0.0079	0.0073	0.0069
Tic-tac-toe	AVE	**0.1998**	0.2170	**0.2154**	0.2162	0.2091	**0.2022**	**0.2114**	0.2245
	STD	0.0063	0.0016	0.0023	0.0038	0.0029	0.0085	0.0076	0.0053
Vote	AVE	0.0709	**0.0465**	0.0597	**0.0440**	0.0542	**0.0336**	0.0493	**0.0368**
	STD	0.0052	0.0053	0.0046	0.0063	0.0036	0.0038	0.0078	0.0053
WaveformEW	AVE	0.2773	**0.2707**	**0.2734**	0.2767	0.2838	**0.2702**	**0.2751**	0.2806
	STD	0.0068	0.0059	0.0081	0.0079	0.0073	0.0057	0.0071	0.0083
WineEW	AVE	**0.0253**	0.0437	0.0279	**0.0228**	**0.0190**	0.0249	0.0288	**0.0267**
	STD	0.0069	0.0052	0.0054	0.0052	0.0087	0.0110	0.0065	0.0056
Zoo	AVE	0.0486	**0.0299**	**0.0440**	0.0605	**0.0427**	0.0446	0.0438	**0.0040**
	STD	0.0080	0.0137	0.0006	0.0059	0.0117	0.0048	0.0009	0.0006
Clean1	AVE	0.1327	**0.1149**	0.1240	**0.1082**	0.1080	**0.1020**	**0.1224**	0.1242
	STD	0.0049	0.0085	0.0073	0.0077	0.0056	0.0082	0.0081	0.0062
Semeion	AVE	**0.0274**	0.0293	0.0304	**0.0295**	**0.0246**	0.0336	0.0259	**0.0238**
	STD	0.0016	0.0016	0.0018	0.0021	0.0018	0.0015	0.0018	0.0018
Colon	AVE	**0.2463**	0.2535	**0.1670**	0.1875	0.2037	**0.1433**	**0.1570**	0.3530
	STD	0.0242	0.0503	0.0379	0.0335	0.0248	0.0286	0.0216	0.1000
Leukemia	AVE	0.0052	**0.0049**	**0.0049**	0.0051	**0.0049**	**0.0049**	0.0429	**0.0365**
	STD	0.0006	0.0000	0.0000	0.0004	0.0000	0.0000	0.0326	0.0328
Ranking	W|T|L	10|0|12	12|0|10	10|0|12	**12|0|10**	10|1|11	10|1|11	10|0|12	12|0|10
Overall Ranking	F-Test	5	4.409	4.9091	**3.8182**	4.0909	4.1364	5.0455	4.5909

Table 12 reveals the average results of proposed methods with S-shaped TFs. The superior accuracies of the BSSA with crossover operator can be detected on majority of datasets. The reason is that it can make a more stable balance between the diversification and intensification leanings due to its effective crossover operator between the candidate salps. Based on the ranking orders, the BSSA with S2 function and crossover strategy is the best algorithm among other optimizers. It is capable of providing higher accuracies than other

optimizers on 68% of the datasets when showing acceptable STD values.

Table 12: Comparison between the BSSA with S-Shaped TFs approaches and the proposed method (with CP) based on the average accuracy.

Benchmark	Stat. Measure	BSSA_S1	BSSA_S1_CP	BSSA_S2	BSSA_S2_CP	BSSA_S3	BSSA_S3_CP	BSSA_S4	BSSA_S4_CP
Breastcancer	AVE	**0.9771**	0.9608	0.9571	**0.9724**	0.9743	**0.9768**	0.9686	**0.9829**
	STD	0.0000	0.0017	0.0000	0.0027	0.0000	0.0010	0.0000	0.0000
BreastEW	AVE	0.9478	**0.9616**	**0.9557**	0.9505	**0.9584**	0.9484	0.9544	**0.9603**
	STD	0.0041	0.0036	0.0036	0.0056	0.0046	0.0035	0.0033	0.0029
Exactly	AVE	**0.9932**	0.9905	0.9891	**0.9963**	0.9663	**0.9803**	**0.9843**	0.9823
	STD	0.0132	0.0125	0.0169	0.0046	0.0332	0.0253	0.0227	0.0209
Exactly2	AVE	0.7239	**0.7480**	0.7392	**0.7509**	0.7560	**0.7582**	**0.7611**	0.7224
	STD	0.0134	0.0078	0.0087	0.0092	0.0000	0.0183	0.0047	0.0078
HeartEW	AVE	**0.8467**	0.8336	0.8257	**0.8338**	0.8104	**0.8605**	0.8395	**0.8432**
	STD	0.0071	0.0050	0.0113	0.0072	0.0096	0.0070	0.0107	0.0073
Lymphography	AVE	**0.8734**	0.8369	0.8113	**0.8410**	0.8491	**0.8900**	0.8455	**0.8707**
	STD	0.0090	0.0093	0.0109	0.0121	0.0113	0.0110	0.0131	0.0085
M-of-n	AVE	0.9960	**0.9976**	0.9977	**0.9987**	0.9869	**0.9918**	0.9887	**0.9941**
	STD	0.0072	0.0066	0.0047	0.0041	0.0181	0.0133	0.0116	0.0076
PenglungEW	AVE	0.8450	**0.9198**	**0.9009**	0.7883	0.8153	**0.8775**	0.8261	**0.9225**
	STD	0.0122	0.0086	0.0164	0.0102	0.0143	0.0137	0.0154	0.0093
SonarEW	AVE	0.8654	**0.9285**	0.8744	**0.8949**	0.8885	**0.9372**	0.8740	**0.8910**
	STD	0.0098	0.0079	0.0113	0.0107	0.0137	0.0097	0.0096	0.0099
SpectEW	AVE	0.8139	**0.8565**	**0.8585**	0.8418	**0.8741**	0.8361	**0.8483**	0.8356
	STD	0.0078	0.0051	0.0084	0.0072	0.0091	0.0054	0.0072	0.0082
CongressEW	AVE	0.9584	**0.9668**	0.9645	**0.9697**	0.9593	**0.9628**	**0.9699**	0.9645
	STD	0.0050	0.0053	0.0047	0.0037	0.0051	0.0035	0.0035	0.0048
IonosphereEW	AVE	**0.9028**	0.8634	0.9241	**0.9286**	**0.9258**	0.9182	0.8892	**0.9034**
	STD	0.0055	0.0059	0.0048	0.0051	0.0068	0.0081	0.0076	0.0058
KrvskpEW	AVE	0.9629	**0.9657**	**0.9711**	0.9661	0.9570	**0.9644**	0.9606	**0.9607**
	STD	0.0048	0.0036	0.0037	0.0046	0.0036	0.0059	0.0055	0.0067
Tic-tac-toe	AVE	0.7871	**0.7902**	**0.7926**	0.7822	0.8086	**0.8205**	0.7789	**0.7939**
	STD	0.0000	0.0065	0.0026	0.0031	0.0045	0.0000	0.0029	0.0033
Vote	AVE	0.9571	**0.9629**	0.9491	**0.9529**	**0.9584**	0.9511	**0.9696**	0.9489
	STD	0.0057	0.0092	0.0057	0.0035	0.0042	0.0059	0.0060	0.0040
WaveformEW	AVE	**0.7379**	0.7337	0.7315	**0.7381**	0.7328	**0.7335**	0.7316	**0.7321**
	STD	0.0039	0.0045	0.0056	0.0060	0.0067	0.0069	0.0052	0.0072
WineEW	AVE	0.9918	**0.9985**	0.9633	**0.9772**	0.9704	**0.9933**	**0.9794**	0.9708
	STD	0.0051	0.0039	0.0051	0.0021	0.0055	0.0056	0.0043	0.0056
Zoo	AVE	**0.9340**	0.9026	**0.9608**	**0.9608**	**1.0000**	**1.0000**	0.9438	**0.9634**
	STD	0.0096	0.0159	0.0000	0.0000	0.0000	0.0000	0.0068	0.0068
Clean1	AVE	0.8462	**0.8894**	0.8969	**0.8999**	**0.8945**	0.8796	**0.8996**	0.8962
	STD	0.0057	0.0067	0.0050	0.0049	0.0060	0.0042	0.0060	0.0068
Semeion	AVE	**0.9783**	0.9749	**0.9762**	0.9721	0.9764	**0.9799**	0.9681	**0.9744**
	STD	0.0014	0.0018	0.0018	0.0018	0.0012	0.0015	0.0018	0.0015
Colon	AVE	**0.8398**	0.7570	0.7398	**0.8656**	**0.7849**	0.6860	0.7129	**0.8785**
	STD	0.0059	0.0164	0.0082	0.0122	0.0155	0.0188	0.0098	0.0139
Leukemia	AVE	0.9311	**0.9933**	0.9733	**1.0000**	**1.0000**	0.9889	**1.0000**	0.9289
	STD	0.0122	0.0203	0.0332	0.0000	0.0000	0.0253	0.0000	0.0169
Ranking	W|T|L	9|0|13	13|0|9	6|1|15	15|1|6	7|1|14	14|1|7	8|0|14	14|0|8
Overall Ranking	F-Test	4.7955	4.0909	5.0455	**3.75**	4.7955	3.9091	5.1818	4.4318

Table 13 tabulates the average accuracy results of the proposed methods with V-shaped TFs. For the best and worst obtained accuracies we refer the reader to Table 25 in the appendix of tables. From Table 13, it is observed that the accuracies have been increased in those cases that utilize both crossover operator and V-shaped transfer formula. For instance, the BSSA_V1_CP, BSSA_V2_CP and BSSA_V4_CP show higher classification rates than those of their competitors on Breastcancer, BreastEW, and Exactly datasets. The enriched searching patterns of algorithms with crossover scheme can be detected from their improved results on different datasets compared to other binary versions. By comparing the BSSA_V3 with BSSA_V3_CP, it is seen that each method has outperformed other one on 11 datasets and both methods have achieved to a similar rank. Regarding the overall ranks, the BSSA_V2_CP can be selected as the best version.

The average number of features found by BSSA-based techniques with S-shaped TFs are revealed in Table 14. As it can be seen, both BSSA_S4 and BSSA_S4_CP are similarly

Table 13: Comparison between the BSSA with V-Shaped TFs approaches and the related version with CP based on average accuracy.

Benchmark	Stat. Measure	BSSA_V1	BSSA_V1_CP	BSSA_V2	BSSA_V2_CP	BSSA_V3	BSSA_V3_CP	BSSA_V4	BSSA_V4_CP
Breastcancer	**AVE**	0.9659	**0.9713**	0.9707	**0.9767**	0.9678	**0.9735**	0.9684	**0.9695**
	STD	0.0025	0.0005	0.0018	0.0017	0.0018	0.0013	0.0007	0.0026
BreastEW	**AVE**	0.9516	**0.9608**	0.9551	**0.9661**	**0.9554**	0.9400	0.9528	**0.9601**
	STD	0.0042	0.0040	0.0046	0.0044	0.0053	0.0049	0.0038	0.0042
Exactly	**AVE**	0.9374	**0.9663**	0.9313	**0.9586**	0.9533	**0.9640**	0.9281	**0.9759**
	STD	0.0665	0.0445	0.0629	0.0526	0.0558	0.0369	0.0625	0.0284
Exactly2	**AVE**	**0.7589**	0.7354	0.7277	**0.7540**	**0.7655**	0.7203	**0.7467**	0.7302
	STD	0.0270	0.0106	0.0119	0.0000	0.0029	0.0089	0.0212	0.0129
HeartEW	**AVE**	0.8217	**0.8262**	0.8089	**0.8316**	**0.8299**	0.8252	**0.8272**	0.8215
	STD	0.0101	0.0108	0.0104	0.0080	0.0071	0.0102	0.0109	0.0104
Lymphography	**AVE**	**0.8644**	0.8459	0.8473	**0.8650**	**0.8203**	0.8068	0.8099	**0.8509**
	STD	0.0125	0.0153	0.0155	0.0151	0.0129	0.0113	0.0154	0.0172
M-of-n	**AVE**	0.9753	**0.9891**	0.9758	**0.9863**	**0.9777**	0.9735	**0.9843**	0.9813
	STD	0.0315	0.0141	0.0315	0.0233	0.0274	0.0368	0.0205	0.0231
PenglungEW	**AVE**	**0.9414**	0.8270	0.8523	**0.9189**	**0.8973**	0.8847	**0.8838**	0.8793
	STD	0.0102	0.0182	0.0154	0.0000	0.0110	0.0173	0.0161	0.0137
SonarEW	**AVE**	**0.8997**	0.8894	**0.9365**	0.9022	0.8910	**0.9016**	0.8465	**0.8974**
	STD	0.0106	0.0126	0.0086	0.0076	0.0119	0.0106	0.0117	0.0114
SpectEW	**AVE**	**0.8306**	0.8072	**0.8465**	0.8236	0.8478	**0.8699**	0.8239	**0.8331**
	STD	0.0056	0.0132	0.0109	0.0101	0.0091	0.0064	0.0093	0.0117
CongressEW	**AVE**	0.9535	**0.9708**	**0.9795**	0.9587	**0.9624**	0.9564	**0.9723**	0.9713
	STD	0.0036	0.0039	0.0056	0.0058	0.0042	0.0055	0.0044	0.0089
IonosphereEW	**AVE**	**0.9331**	0.9106	**0.9305**	0.8938	**0.9487**	0.9136	0.9021	**0.9078**
	STD	0.0074	0.0067	0.0110	0.0097	0.0053	0.0086	0.0081	0.0069
KrvskpEW	**AVE**	0.9523	**0.9540**	**0.9529**	0.9447	0.9479	**0.9536**	**0.9546**	0.9525
	STD	0.0086	0.0097	0.0072	0.0071	0.0068	0.0081	0.0074	0.0072
Tic-tac-toe	**AVE**	**0.8052**	0.7868	**0.7895**	0.7875	0.7947	**0.8025**	**0.7933**	0.7800
	STD	0.0074	0.0011	0.0020	0.0034	0.0027	0.0086	0.0076	0.0054
Vote	**AVE**	0.9324	**0.9558**	0.9433	**0.9589**	0.9500	**0.9696**	0.9536	**0.9662**
	STD	0.0057	0.0054	0.0045	0.0063	0.0042	0.0042	0.0075	0.0055
WaveformEW	**AVE**	0.7255	**0.7321**	**0.7291**	0.7256	0.7190	**0.7323**	**0.7271**	0.7219
	STD	0.0068	0.0058	0.0077	0.0077	0.0072	0.0058	0.0071	0.0082
WineEW	**AVE**	**0.9794**	0.9610	0.9768	**0.9820**	**0.9858**	0.9794	0.9753	**0.9779**
	STD	0.0073	0.0057	0.0051	0.0056	0.0093	0.0111	0.0069	0.0055
Zoo	**AVE**	0.9562	**0.9739**	**0.9608**	0.9431	**0.9621**	0.9595	0.9608	**1.0000**
	STD	0.0084	0.0139	0.0000	0.0060	0.0114	0.0050	0.0000	0.0000
Clean1	**AVE**	0.8706	**0.8882**	0.8793	**0.8955**	0.8955	**0.9020**	**0.8805**	0.8793
	STD	0.0050	0.0082	0.0071	0.0076	0.0055	0.0084	0.0079	0.0061
Semeion	**AVE**	**0.9774**	0.9754	0.9742	**0.9751**	**0.9801**	0.9710	0.9789	**0.9808**
	STD	0.0017	0.0016	0.0019	0.0021	0.0019	0.0013	0.0017	0.0018
Colon	**AVE**	**0.7538**	0.7473	**0.8344**	0.8140	0.7978	**0.8581**	**0.8441**	0.6462
	STD	0.0232	0.0495	0.0367	0.0325	0.0239	0.0276	0.0209	0.0993
Leukemia	**AVE**	**1.0000**	**1.0000**	**1.0000**	**1.0000**	**1.0000**	**1.0000**	0.9622	**0.9689**
	STD	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0336	0.0338
Ranking	W|T|L	10|1|11	11|1|10	9|1|12	12|1|9	11|1|10	10|1|11	10|0|12	12|0|10
Overall Ranking	F-Test	4.9318	4.4545	4.9091	**3.8409**	4.1591	4.1591	4.9318	4.6136

the best choices in terms of selected features.

Table 14: Comparison between the BSSA based S-Shaped transfer functions approaches and the proposed method (with CP) based on average number of features.

Benchmark	Stat. Measure	BSSA_S1	BSSA_S1_CP	BSSA_S2	BSSA_S2_CP	BSSA_S3	BSSA_S3_CP	BSSA_S4	BSSA_S4_CP
Breastcancer	**AVE**	6.0000	**5.2333**	4.6333	**3.4333**	4.8000	**3.8667**	**4.7333**	5.2000
	STD	0.0000	0.4302	0.4901	0.5040	1.3493	0.3457	0.9803	0.4068
BreastEW	**AVE**	**19.8333**	20.5000	**17.2000**	18.3667	**16.0000**	16.7000	16.0667	**14.8333**
	STD	2.1669	1.7568	2.5380	2.8099	2.3342	2.3364	2.6121	1.8770
Exactly	**AVE**	6.9667	**6.8000**	7.0000	**6.7000**	7.4000	**7.2000**	**7.2000**	7.3333
	STD	0.6687	0.5509	0.6433	0.4661	0.7701	0.6644	0.6644	0.6065
Exactly2	**AVE**	9.2000	**8.6333**	8.7333	**6.0333**	**2.0333**	2.7333	**1.8000**	9.1333
	STD	2.7342	1.6291	0.7397	2.6193	0.7649	2.3916	1.2972	1.0743
HeartEW	**AVE**	**6.9667**	8.3000	7.0000	**6.0000**	8.0333	**5.8000**	6.8333	**6.6667**
	STD	1.6291	0.5350	1.4622	1.3646	1.2726	1.4239	1.2058	1.3218
Lymphography	**AVE**	13.1333	**10.8000**	**9.9000**	10.0000	**10.2333**	10.2667	9.9667	**9.4667**
	STD	1.1366	0.9613	1.3734	1.2318	1.7357	1.9286	1.5196	1.8333
M-of-n	**AVE**	6.9333	**6.8333**	7.0333	**6.7333**	7.2667	**7.1000**	**7.2000**	7.3000
	STD	0.6915	0.5307	0.5561	0.6397	0.6397	0.6618	0.7144	0.6513
PenglungEW	**AVE**	**189.5000**	193.5000	195.4333	**166.8333**	172.7333	**171.6000**	167.7000	**159.9000**
	STD	25.5920	19.3333	10.7405	15.1887	9.1234	9.9329	7.9791	5.9385
SonarEW	**AVE**	42.2667	**41.1333**	39.8667	**35.6667**	**32.7333**	33.3667	**30.7667**	31.1000
	STD	3.0954	3.6173	4.4313	2.9866	2.6253	2.8585	3.3081	2.6044
SpectEW	**AVE**	**11.8000**	12.7667	**12.0000**	14.4667	13.3000	**10.9333**	**10.6333**	11.0333
	STD	2.1877	1.6121	2.3342	2.4457	2.0703	3.5809	2.3413	1.6709
CongressEW	**AVE**	8.1333	**7.4000**	**7.0333**	7.2000	**5.4333**	5.7333	5.9333	**5.5333**
	STD	1.2521	1.6103	2.2047	1.8644	1.4547	1.3629	1.4840	1.6965
IonosphereEW	**AVE**	22.0333	**20.8333**	18.9000	**18.8333**	17.2667	**15.8667**	**14.3667**	14.9333
	STD	3.5862	2.4925	2.3831	2.5875	3.0731	2.5829	2.3706	2.4486
KrvskpEW	**AVE**	**25.6667**	25.7333	22.2667	**21.9667**	21.9000	**20.4667**	21.6000	**20.5667**
	STD	2.1549	2.1324	2.1324	2.3706	2.3976	2.5560	2.4719	2.3735
Tic-tac-toe	**AVE**	6.0000	**5.2333**	6.0000	**5.9000**	6.9000	**6.0000**	5.2667	**5.2000**
	STD	0.0000	0.5040	0.0000	0.3051	0.3051	0.0000	0.6915	0.4842
Vote	**AVE**	**7.4667**	8.4667	**5.9667**	9.0333	7.1333	**4.8333**	**5.7667**	6.9000
	STD	1.2521	1.4077	1.5862	1.5421	2.1772	1.4875	1.8696	1.8634
WaveformEW	**AVE**	30.4333	**28.7667**	**25.4000**	25.8333	23.3333	**22.9000**	24.0667	**23.6000**
	STD	2.0457	2.6997	2.8357	2.6663	2.6305	3.3255	2.7409	3.0468
WineEW	**AVE**	**7.6333**	8.1333	**6.3667**	6.8333	7.9667	**6.3333**	**6.8333**	7.8667
	STD	0.8087	1.6554	1.1592	1.2617	2.0924	0.9589	1.3917	2.1772
Zoo	**AVE**	**8.1333**	8.2000	9.2667	**7.9333**	7.5667	**6.7000**	8.3333	**6.1667**
	STD	0.8996	1.1567	0.7849	0.7397	0.7739	0.7022	1.0613	0.8743
Clean1	**AVE**	**115.5667**	120.0667	103.5667	**99.7333**	93.2333	**92.1667**	89.5000	**86.4000**
	STD	13.1193	8.4115	7.4772	6.6381	8.7678	6.2427	5.6614	7.2853
Semeion	**AVE**	**190.0333**	196.9000	166.2333	**165.9000**	148.1333	**147.5000**	**140.8000**	143.2000
	STD	23.1181	10.3968	8.0288	14.5705	7.3940	8.7168	9.7994	7.2844
Colon	**AVE**	**984.9000**	1160.8333	**1079.4333**	1180.7000	**1093.0000**	1097.4333	**1044.6667**	1049.2333
	STD	17.4224	152.8493	105.4853	85.4312	36.7283	44.7165	31.5391	22.2272
Leukemia	**AVE**	4382.8000	**4063.0333**	4159.2670	**3642.5000**	**3491.8670**	3959.9333	**3501.6670**	4326.3667
	STD	415.7237	482.5962	346.0309	235.9664	31.9145	530.6809	23.3036	515.6235
Ranking	W|T|L	11|0|11	11|0|11	8|0|14	14|0|8	7|0|15	15|0|7	12|0|10	10|0|12
Overall Ranking	F-Test	6.1364	6.2727	5.1818	4.5227	4.5455	3.2500	**3.0455**	**3.0455**

Inspecting the average number of features attained by BSSA-based algorithms with V-shaped TFs in Table 15, we can notice that the BSSA_V2_CP version has obtained the best place among other versions. The reason is that the crossover operator has enhanced the searching competences of the BSSA_V2_CP on majority of tasks.

Average running time of BSSA-based optimizers with S-shaped TFs are shown in Table 16. Inspecting the results in in this table, the BSSA_S3_CP is the best approach among others. On the other hand, Table 17 compares the the running time of the BSSA-based algorithms with V-shaped TFs.It can be noticed that the BSSA_V4_CP algorithm has the lowest average running time. From the running time results in Tables 16 and 17, it is evident that BSSA-based versions that utilize the crossover strategy beside the S-shaped and V-shaped TFs can perform the exploration and exploitation phases better and quicker than other binary versions that still employ the average operator of the basic SSA.

Table 15: Comparison between the BSSA based V-Shaped transfer functions approaches and the proposed method (with CP) based on average number of features.

Benchmark	Stat. Measure	BSSA_V1	BSSA_V1_CP	BSSA_V2	BSSA_V2_CP	BSSA_V3	BSSA_V3_CP	BSSA_V4	BSSA_V4_CP
Breastcancer	**AVE**	5.0000	**4.2667**	5.0667	**4.2000**	**5.2333**	5.5667	**6.2333**	6.2667
	STD	0.7428	0.4498	0.9072	0.5509	0.5040	0.7739	0.4302	0.4498
BreastEW	**AVE**	14.5333	**14.0000**	**13.4333**	14.8333	13.8333	**13.6667**	**11.9333**	15.1667
	STD	2.8129	2.5052	3.4309	3.1082	3.6111	2.9165	3.2898	2.4925
Exactly	**AVE**	7.7000	**7.3333**	7.8667	**7.4000**	7.7000	**7.4000**	7.7333	**7.3000**
	STD	1.0222	0.8023	0.9371	0.9685	1.0875	0.7701	1.0483	0.7497
Exactly2	**AVE**	**1.9000**	2.4667	6.7667	**1.6000**	**1.8667**	9.0333	**3.8667**	7.2667
	STD	1.0619	2.9212	2.4591	0.6215	0.8996	1.0334	3.3501	2.1961
HeartEW	**AVE**	7.9333	**6.0000**	**6.1000**	**6.1000**	6.4667	**6.2333**	7.5000	**6.8667**
	STD	1.8182	1.2318	1.5166	0.9948	1.7564	0.8584	1.4081	1.0743
Lymphography	**AVE**	**9.1667**	10.0333	**8.1333**	8.2667	8.1000	**8.0333**	**7.3333**	7.9000
	STD	2.8416	2.4980	3.0820	1.8742	2.9167	1.9911	2.1227	1.9538
M-of-n	**AVE**	7.7333	**7.1667**	7.7333	**7.2667**	7.3333	**7.2333**	**7.4333**	7.4667
	STD	0.8683	0.9129	1.0148	0.8683	1.0283	0.9714	0.9353	0.8604
PenglungEW	**AVE**	133.8667	**127.2000**	**111.0333**	133.3333	**103.1333**	133.7000	**109.1667**	137.4333
	STD	40.3431	44.5633	54.1113	26.1116	55.9715	37.5014	50.0221	32.8210
SonarEW	**AVE**	30.3667	**26.7667**	30.6667	**27.9667**	**28.1667**	28.3333	**27.6333**	28.1667
	STD	3.2641	4.8187	4.3417	3.3475	4.2757	4.2209	4.7524	3.5143
SpectEW	**AVE**	**6.5000**	8.7000	11.1667	**5.5667**	**9.3333**	10.8667	10.2667	**8.9000**
	STD	3.6742	1.8597	2.2907	2.8367	2.5371	2.4031	2.0331	2.3831
CongressEW	**AVE**	**3.5333**	4.5333	7.3333	**4.6333**	6.9000	**4.0000**	4.4667	**3.4667**
	STD	2.2854	1.7953	1.9885	1.8659	1.6474	2.1335	1.9954	1.4794
IonosphereEW	**AVE**	14.2667	**13.3000**	13.7000	**12.6333**	14.2667	**10.5333**	12.5000	**12.2000**
	STD	2.7535	4.1784	3.5926	3.4887	3.3107	3.5597	3.5307	4.6416
KrvskpEW	**AVE**	**18.2000**	18.9667	**18.4667**	20.2333	**18.3000**	18.8667	**18.2000**	18.3000
	STD	4.4443	3.0680	3.0141	2.5688	3.4356	3.0820	3.4978	4.0442
Tic-tac-toe	**AVE**	6.2333	**5.3000**	6.3000	**5.2000**	**5.2667**	6.0000	6.0667	**6.0333**
	STD	0.8584	0.5960	0.9154	0.4068	0.5208	0.0000	0.3651	0.3198
Vote	**AVE**	6.3667	**4.4000**	5.7000	**5.3000**	7.4667	**5.4667**	**5.3333**	5.3667
	STD	2.0592	2.1592	2.4233	1.3684	2.7759	1.5698	2.0734	2.6972
WaveformEW	**AVE**	22.0667	**21.9667**	20.7000	**20.0667**	22.4333	**20.7333**	**19.6333**	21.2000
	STD	3.7318	3.0680	4.1369	3.1724	4.1163	4.2825	3.2322	3.9862
WineEW	**AVE**	**6.4333**	6.6667	**6.3667**	6.5667	6.4000	**5.8000**	**5.6333**	6.2667
	STD	1.6333	1.2130	1.8286	1.6121	1.5669	1.1861	1.0662	1.8742
Zoo	**AVE**	8.4333	**6.4333**	8.2667	**6.7000**	8.2000	**7.1667**	7.9667	**6.4667**
	STD	1.4308	1.0400	0.9444	0.9879	1.4239	1.5775	1.3767	0.8996
Clean1	**AVE**	76.7000	**70.8333**	**75.1000**	78.7667	**75.5000**	81.4333	**68.9667**	77.6667
	STD	13.0758	17.5540	14.8982	13.3563	16.6604	8.3900	16.7507	9.8483
Semeion	**AVE**	134.4000	**130.1333**	129.4667	**128.8000**	131.4000	**129.2000**	132.2333	**127.8667**
	STD	7.7797	13.9747	17.6728	14.5232	7.3700	12.9679	13.6904	12.5003
Colon	**AVE**	**502.8333**	675.1333	**608.8000**	660.2333	710.2333	**562.2000**	**533.2333**	552.6333
	STD	426.8525	394.4688	418.4239	367.4116	393.4634	391.4070	381.6319	441.3998
Leukemia	**AVE**	3709.9670	**3524.5333**	**3503.2670**	3629.9000	3506.8670	**3496.7000**	**3953.0670**	4070.5667
	STD	398.4409	27.50643	25.7266	279.0204	25.2870	31.9160	632.9743	608.5844
Ranking	W|T|L	7|0|15	15|0|7	8|1|13	13|1|8	8|0|14	14|0|8	14|0|8	8|0|14
Overall Ranking	F-Test	5.5000	4.0000	5.1818	**3.8182**	4.8636	4.4773	3.8864	4.2727

Table 16: Comparison between the BSSA with S-shaped TFs and the related version with CP based on the average running time.

Benchmark	Stat. Measure	BSSA_S1	BSSA_S1_CP	BSSA_S2	BSSA_S1_CP	BSSA_S3	BSSA_S3_CP	BSSA_S4	BSSA_S4_CP
Breastcancer	**AVE**	6.3419	**6.0842**	6.1287	**5.8927**	6.0900	**5.8258**	6.0691	**5.8422**
	STD	0.2242	0.1260	0.1176	0.1250	0.1593	0.1478	0.1416	0.1384
BreastEW	**AVE**	6.9568	**6.6689**	6.8192	**6.4934**	6.7886	**6.4352**	6.7479	**6.4043**
	STD	0.1544	0.1272	0.1412	0.1214	0.1368	0.1305	0.1365	0.1298
Exactly	**AVE**	9.1079	**8.3701**	8.8297	**7.9362**	8.7315	**8.1474**	8.5636	**7.5922**
	STD	0.1820	0.2866	0.1895	0.1775	0.1461	0.1931	0.1479	0.1858
Exactly2	**AVE**	9.2486	**9.0258**	8.9892	**8.4106**	8.6881	**7.9427**	8.6479	**8.0397**
	STD	0.2807	0.3479	0.1765	0.2986	0.1530	0.2523	0.1408	0.2022
HeartEW	**AVE**	**4.8109**	4.9190	**4.7856**	4.9095	**4.8080**	4.8747	**4.7876**	4.8858
	STD	0.1153	0.1310	0.1266	0.1480	0.1547	0.1283	0.1490	0.1209
Lymphography	**AVE**	**4.5691**	4.6471	**4.6016**	4.6431	**4.5918**	4.6382	**4.5776**	4.6911
	STD	0.1373	0.0935	0.1310	0.1394	0.1321	0.1233	0.1051	0.1106
M-of-n	**AVE**	8.9426	**8.8660**	8.7137	**7.9496**	8.5289	**7.6689**	8.4811	**7.5729**
	STD	0.1567	0.2029	0.1353	0.2322	0.1652	0.2028	0.1800	0.1634
PenglungEW	**AVE**	6.9319	**6.9308**	7.0017	**6.9442**	6.9723	**6.9286**	6.9908	**6.9542**
	STD	0.1779	0.1783	0.2111	0.1706	0.1598	0.1928	0.1647	0.1729
SonarEW	**AVE**	5.2936	**5.2555**	5.2877	**5.2270**	5.2625	**5.1872**	5.2572	**5.1788**
	STD	0.1417	0.1166	0.1429	0.1409	0.1502	0.1487	0.1306	0.1277
SpectEW	**AVE**	**4.8724**	4.9135	**4.8749**	4.9194	**4.9058**	4.9259	**4.8595**	4.9371
	STD	0.1254	0.1146	0.1179	0.1217	0.1166	0.1282	0.0954	0.1070
CongressEW	**AVE**	**5.4705**	5.5734	**5.4873**	5.5849	**5.4636**	5.5814	**5.4580**	5.5357
	STD	0.1292	0.1390	0.0989	0.1287	0.0971	0.1323	0.1208	0.1162
IonosphereEW	**AVE**	5.5331	**5.4944**	5.5000	**5.4048**	5.4766	**5.3749**	5.4798	**5.3395**
	STD	0.1344	0.1425	0.1397	0.1628	0.1002	0.1283	0.1013	0.1139
KrvskpEW	**AVE**	90.1701	**77.9537**	85.5203	**68.7881**	83.3227	**64.0376**	82.4860	**63.1520**
	STD	1.0019	1.8611	0.6986	1.4156	0.7765	0.9309	0.7200	0.6287
Tic-tac-toe	**AVE**	8.8671	**7.6934**	8.6742	**7.3372**	8.4558	**7.0290**	8.4044	**6.8724**
	STD	0.1682	0.2195	0.1747	0.1880	0.1625	0.1509	0.1808	0.1567
Vote	**AVE**	**4.9164**	4.9854	**4.9204**	4.9754	**4.8939**	4.9979	**4.9023**	4.9976
	STD	0.1268	0.1245	0.1445	0.1381	0.1002	0.1326	0.1203	0.1325
WaveformEW	**AVE**	233.4317	**200.5977**	219.4103	**175.3999**	211.4342	**158.3204**	209.5122	**155.2800**
	STD	2.6403	6.1824	2.4184	2.7815	1.5368	2.0943	1.6556	2.0963
WineEW	**AVE**	**4.5797**	4.6636	**4.5874**	4.6801	**4.5819**	4.6498	**4.5683**	4.6587
	STD	0.1356	0.1263	0.1068	0.1127	0.1281	0.1167	0.1213	0.1074
Zoo	**AVE**	**4.5614**	4.6952	**4.5935**	4.6181	**4.5761**	4.5942	**4.5770**	4.6478
	STD	0.1179	0.1546	0.1361	0.0939	0.1149	0.1210	0.1313	0.1266
Clean1	**AVE**	14.5884	**13.1172**	14.0300	**11.9863**	13.6366	**11.2840**	13.5364	**11.0792**
	STD	0.3487	0.4052	0.3311	0.3728	0.3186	0.2966	0.3236	0.2654
Semeion	**AVE**	171.5068	**147.1775**	160.8404	**124.0739**	152.9361	**109.3973**	150.4326	**105.0623**
	STD	2.6292	2.1649	1.4173	2.3551	1.2590	1.2306	1.1394	1.0139
Colon	**AVE**	18.7257	**18.4842**	19.0884	**18.7992**	19.2046	**18.7866**	19.2324	**18.8292**
	STD	0.5844	0.6246	0.5838	0.6407	0.6449	0.6070	0.6399	0.5785
Leukemia	**AVE**	29.0596	**26.5747**	26.0303	**23.4061**	24.4623	**22.6561**	24.5787	**23.5067**
	STD	2.3031	1.5675	2.4104	1.3921	1.2403	0.8432	1.1275	1.3120
Ranking	W|T|L	7|0|15	15|0|7	7|0|15	15|0|7	7|0|15	15|0|7	7|0|15	15|0|7
Overall Ranking	F-Test	5.5455	5	5.8182	4.2273	4.7727	**3.1818**	4.1364	3.3182

Table 17: Comparison between the BSSA with V-shaped TFs and the related version with CP based on the average running time.

Benchmark	Stat. Measure	BSSA_V1	BSSA_V1_CP	BSSA_V2	BSSA_V2_CP	BSSA_V3	BSSA_V3_CP	BSSA_V4	BSSA_V4_CP
Breastcancer	**AVE**	6.0650	**5.7544**	6.0793	**5.7602**	6.0087	**5.7671**	6.0535	**5.7707**
	STD	0.1542	0.1289	0.1310	0.1426	0.1391	0.1570	0.1472	0.1640
BreastEW	**AVE**	6.7490	**6.3354**	6.7242	**6.3116**	6.7241	**6.3232**	6.7204	**6.3470**
	STD	0.1548	0.1459	0.1054	0.1351	0.1468	0.1484	0.1474	0.1219
Exactly	**AVE**	8.4290	**7.6049**	8.3918	**7.4452**	8.3905	**7.4395**	8.4522	**7.4230**
	STD	0.1691	0.2045	0.1605	0.2518	0.1509	0.2402	0.1756	0.2597
Exactly2	**AVE**	8.5800	**7.5672**	8.5698	**7.8250**	8.6158	**7.7201**	8.5339	**7.6678**
	STD	0.2083	0.3811	0.1446	0.2409	0.1493	0.2561	0.1533	0.2616
HeartEW	**AVE**	**4.7885**	4.8539	**4.7795**	4.8300	**4.8058**	4.8155	**4.7629**	4.8385
	STD	0.1485	0.1311	0.1241	0.1015	0.1435	0.1115	0.1143	0.1123
Lymphography	**AVE**	**4.5928**	4.6688	**4.5818**	4.6317	**4.5852**	4.6490	**4.5817**	4.6382
	STD	0.1266	0.1233	0.1128	0.1087	0.1135	0.1077	0.1230	0.0884
M-of-n	**AVE**	8.4435	**7.2751**	8.3370	**7.4175**	8.3191	**7.2508**	8.2535	**7.6105**
	STD	0.1867	0.1895	0.1428	0.2362	0.1603	0.1931	0.1564	0.2569
PenglungEW	**AVE**	7.0545	**6.9564**	6.8316	**6.7616**	6.7966	**6.7419**	6.7937	**6.6936**
	STD	0.2331	0.2646	0.1739	0.1747	0.1856	0.1600	0.1474	0.1582
SonarEW	**AVE**	5.2337	**5.1523**	5.1985	**5.0872**	5.1945	**5.0950**	5.2115	**5.0919**
	STD	0.1504	0.1522	0.1372	0.1406	0.1408	0.1247	0.1676	0.1285
SpectEW	**AVE**	**4.8817**	4.9277	**4.8618**	4.8828	**4.8952**	4.9308	**4.8630**	4.9191
	STD	0.1349	0.1027	0.1129	0.1766	0.0963	0.1359	0.1024	0.1295
CongressEW	**AVE**	**5.4406**	5.5259	**5.4539**	5.5105	**5.4404**	5.5259	**5.4507**	5.5099
	STD	0.1466	0.1534	0.1434	0.1330	0.1103	0.1333	0.1372	0.1388
IonosphereEW	**AVE**	5.5120	**5.2989**	5.4691	**5.2922**	5.4667	**5.3063**	5.4471	**5.2993**
	STD	0.1217	0.1163	0.1286	0.1378	0.1224	0.1478	0.1224	0.1135
KrvskpEW	**AVE**	80.9167	**60.0669**	80.8368	**60.1490**	80.9479	**60.1087**	80.7104	**59.9048**
	STD	0.7489	1.9395	0.9229	1.3245	0.8432	1.6498	0.8994	1.7692
Tic-tac-toe	**AVE**	8.3256	**6.7029**	8.2557	**6.6715**	8.3069	**6.7194**	8.2683	**6.6701**
	STD	0.1533	0.1740	0.1268	0.2075	0.1958	0.2127	0.1660	0.2105
Vote	**AVE**	**4.8986**	4.9969	**4.8907**	4.9518	**4.8872**	4.9493	**4.8821**	4.9461
	STD	0.1053	0.1116	0.1177	0.0960	0.1121	0.1186	0.1202	0.1339
WaveformEW	**AVE**	203.5272	**145.8042**	203.0986	**143.8175**	203.7187	**144.2169**	203.3405	**145.0240**
	STD	2.0957	4.3338	1.9709	4.7723	2.3329	4.6742	2.0857	5.2775
WineEW	**AVE**	**4.5612**	4.6379	**4.5252**	4.6144	**4.5425**	4.6346	**4.5563**	4.6068
	STD	0.1273	0.1251	0.0992	0.1138	0.1021	0.1100	0.1120	0.1015
Zoo	**AVE**	**4.5990**	4.6112	**4.5575**	4.5993	**4.5501**	4.5919	**4.5438**	4.6045
	STD	0.1089	0.1086	0.1098	0.1000	0.1355	0.1224	0.1457	0.1091
Clean1	**AVE**	13.2981	**10.3848**	13.1682	**10.3065**	13.2241	**10.3193**	13.1324	**10.3543**
	STD	0.3548	0.2905	0.3357	0.2838	0.3146	0.3637	0.3455	0.3244
Semeion	**AVE**	145.3891	**93.8624**	145.4128	**94.7978**	145.8595	**94.1344**	145.3749	**93.3334**
	STD	1.8617	4.2413	1.7401	3.6139	1.5058	3.1943	1.5577	3.7049
Colon	**AVE**	19.3587	**18.8523**	18.1871	**17.6476**	18.1081	**17.5061**	18.0409	**17.5174**
	STD	0.9240	0.9281	0.5712	0.5006	0.5278	0.4838	0.5719	0.5925
Leukemia	**AVE**	26.8454	**22.7709**	26.4626	**23.9507**	28.1687	**22.3894**	27.0976	**25.0805**
	STD	1.3364	1.0506	0.8502	2.1127	2.0315	1.6292	1.3519	1.8981
Ranking	W|T|L	7|0|15	15|0|7	7|0|15	15|0|7	7|0|15	15|0|7	7|0|15	15|0|7
Overall Ranking	F-Test	6.2727	4.75	5.0455	3.4545	5.1818	3.7045	4.2273	**3.3636**

To detect the best binary variant among the evaluated versions, the overall ranks are considered here. Table 18 shows the ranks of different binary approaches in terms of different measures based on F-test.

Based on the overall ranks in Table 18, it can be observed that the BSSA_S3_CP has achieved to the lowest rank among others in terms of fitness and accuracy measures over all 22 datasets. According to the number of features and running time results, the BSSA_V2_CP has outperformed other versions. The notable changes in the results show the noteworthy effect of the TF on the effectiveness of the investigated versions. In addition, from the overall results, it can be noticed that the crossover scheme has heightened the efficacy of the related algorithms with both S-shaped and V-shaped TFs in terms of fitness and accuracy measures. The reason is that it has avoided the algorithms from converging towards local solutions to some extent and increased the exploration capacities of proposed BSSA-based approaches in tackling more complex scenarios. Hence, they can establish a more stable tradeoff between the exploration and exploitation trends.

Table 18: Overall Ranking results using the F-test for all proposed approaches based on fitness, accuracy, Number of features and running time.

Algorithm	Fitness	Accuracy	Features	Time
BSSA-S1	8.9545	8.6136	12.8636	11.7727
BSSA-S1-CP	7.7273	7.1364	12.9091	11.3636
BSSA-S2	9.5227	8.9091	11.4545	12.2273
BSSA-S2-CP	6.9545	6.8864	10.4545	9.7273
BSSA-S3	8.1364	8.0682	11.2500	11.2727
BSSA-S3-CP	**6.1364**	**6.2500**	8.4773	8.3864
BSSA-S4	9.2727	9.2273	8.9773	10.1364
BSSA-S4-CP	7.1818	7.2500	9.2045	8.8182
BSSA-V1	9.6364	9.6818	7.6364	9.9545
BSSA-V1-CP	8.8864	9.2727	5.2273	6.9318
BSSA-V2	9.5455	9.7727	7.5227	7.0909
BSSA-V2-CP	8.0909	8.3409	**4.8864**	**4.7273**
BSSA-V3	8.2273	8.4091	6.9091	7.3636
BSSA-V3-CP	8.5682	8.8409	6.2045	5.2045
BSSA-V4	10.1591	10.2273	5.9318	6.2273
BSSA-V4-CP	9.0000	9.1136	6.0909	4.7955

Table 19 reveals the attained p-values for the BSSA_S3_CP compared to other optimizers.

Table 19: The p-values of the Wilcoxon test of BSSA_S3_CP fitness results vs. other approaches ($p \geq 0.05$ are underlined).

Benchmark	BSSA_S1	BSSA_S1_CP	BSSA_S2	BSSA_S2_CP	BSSA_S3	BSSA_S4	BSSA_S4_CP	BSSA_V1	BSSA_V1_CP	BSSA_V2	BSSA_V2_CP	BSSA_V3	BSSA_V3_CP	BSSA_V4	BSSA_V4_CP
Breastcancer	8.64E-14	2.69E-12	1.43E-12	4.92E-11	9.50E-13	1.43E-12	6.33E-13	2.90E-12	1.15E-12	2.35E-12	7.76E-02	2.05E-12	9.99E-13	9.90E-13	1.90E-12
BreastEW	9.88E-02	3.77E-11	2.22E-09	6.20E-01	5.12E-11	1.94E-08	2.90E-11	1.28E-03	2.92E-11	1.05E-09	2.93E-11	1.80E-07	3.14E-08	7.26E-08	2.94E-11
Exactly	1.34E-03	3.02E-01	1.16E-01	1.92E-02	1.10E-01	1.72E-01	5.07E-01	1.62E-02	5.82E-01	3.97E-03	1.69E-01	4.08E-01	4.04E-02	1.02E-03	6.50E-01
Exactly2	1.57E-09	5.94E-04	4.50E-05	2.71E-02	3.35E-04	2.95E-04	3.19E-09	4.20E-05	3.22E-05	2.52E-07	3.13E-04	3.34E-04	2.42E-09	9.09E-06	5.69E-07
HeartEW	9.73E-07	1.32E-11	5.15E-11	1.05E-10	2.72E-11	4.13E-10	1.08E-09	2.74E-11	4.97E-11	2.78E-11	6.57E-11	3.05E-11	3.97E-11	4.09E-11	3.17E-11
Lymphography	5.60E-10	2.84E-11	2.92E-11	2.91E-11	4.84E-11	4.40E-11	2.67E-07	1.83E-08	2.90E-11	6.95E-11	5.54E-07	2.95E-11	2.94E-11	2.96E-11	1.98E-09
M-of-n	4.49E-01	8.91E-02	3.81E-01	1.20E-02	1.74E-01	1.19E-01	5.09E-01	9.87E-03	8.20E-01	2.93E-02	6.22E-01	8.33E-02	4.83E-02	2.19E-01	8.08E-02
PenglungEW	6.65E-11	3.48E-11	6.22E-03	2.97E-11	6.61E-11	4.25E-11	2.94E-11	2.99E-11	2.12E-09	9.50E-04	2.97E-11	2.99E-11	4.07E-05	1.69E-05	6.89E-04
SonarEW	2.98E-11	8.09E-07	2.98E-11	3.28E-11	3.45E-11	2.97E-11	2.96E-11	3.98E-11	4.03E-11	2.83E-01	2.95E-11	4.02E-11	5.41E-11	2.99E-11	3.29E-11
SpectEW	9.13E-11	2.89E-11	2.93E-11	2.40E-02	2.89E-11	4.02E-09	4.82E-01	1.18E-03	2.78E-10	1.84E-05	2.23E-05	3.10E-09	2.92E-11	1.08E-06	4.96E-01
CongressEW	4.28E-06	9.71E-02	3.70E-01	4.84E-07	1.59E-02	3.17E-08	8.00E-02	4.23E-09	4.09E-10	5.18E-11	2.89E-02	5.10E-02	1.44E-04	2.81E-10	2.33E-05
IonosphereEW	2.69E-10	2.98E-11	5.75E-03	4.37E-06	4.08E-04	5.18E-11	1.23E-08	9.57E-09	3.17E-03	5.04E-06	3.31E-09	2.97E-11	3.25E-01	5.26E-08	1.10E-04
KrvskpEW	3.09E-02	5.69E-01	3.15E-05	4.33E-01	5.37E-07	6.81E-03	1.47E-02	9.52E-07	6.15E-05	3.25E-07	1.26E-10	1.85E-09	1.33E-06	5.86E-06	5.80E-07
Tic-tac-toe	1.69E-14	1.57E-13	4.16E-14	6.13E-14	6.12E-14	3.15E-13	1.19E-13	6.75E-13	2.03E-13	5.67E-13	1.55E-13	2.54E-13	3.15E-13	6.37E-13	3.17E-13
Vote	2.12E-02	7.61E-05	2.37E-02	6.89E-01	1.07E-04	2.61E-10	3.14E-03	3.70E-11	9.78E-04	1.08E-06	1.21E-04	4.40E-02	3.96E-11	3.62E-01	5.07E-10
WaveformEW	9.33E-02	3.37E-01	9.77E-02	3.64E-02	5.64E-01	1.54E-01	4.04E-01	7.20E-05	4.29E-01	8.50E-02	7.49E-04	2.39E-08	6.84E-01	1.10E-02	3.44E-06
WineEW	6.23E-04	1.85E-01	2.46E-11	2.21E-11	2.41E-11	2.18E-11	2.25E-11	1.31E-09	2.50E-11	6.33E-10	3.55E-08	2.19E-03	7.51E-05	9.16E-10	2.00E-09
Zoo	1.29E-11	1.60E-11	9.91E-12	9.64E-12	7.52E-05	1.47E-11	1.16E-11	1.59E-11	9.30E-08	1.29E-11	1.29E-11	1.62E-11	1.57E-11	1.49E-11	2.56E-01
Clean1	3.00E-11	6.28E-06	3.00E-11	3.01E-11	2.14E-10	3.00E-11	3.66E-11	4.43E-07	2.11E-07	6.63E-01	3.01E-11	3.33E-11	3.01E-11	1.67E-01	4.96E-01
Semeion	8.11E-09	3.01E-11	3.14E-10	3.02E-11	3.47E-10	3.01E-11	3.67E-11	4.21E-05	2.43E-09	9.90E-11	4.98E-09	8.77E-02	3.01E-11	1.96E-01	4.21E-04
Colon	2.97E-11	3.01E-11	2.99E-11	3.00E-11	2.99E-11	3.00E-11	2.99E-11	3.00E-11	3.01E-11	3.01E-11	3.01E-11	3.00E-11	3.00E-11	3.01E-11	1.44E-03
Leukemia	3.45E-02	3.00E-11	2.99E-11	3.00E-11	2.98E-11	4.75E-10	4.03E-11	3.00E-11	3.00E-11	3.00E-11	3.00E-11	3.00E-11	3.00E-11	4.08E-06	3.00E-11

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From Table 19, the p-values are below 0.05 for majority of cases, while for 39 cases, the they are bigger than 0.05. Therefore, the improvements in the results of the BSSA_S3_CP are statistically superior to those of other versions in dealing with majority of the datasets, which verifies the efficacy of this algorithm.

Due to the importance of the classification accuracy and fitness results in dealing with the feature selection tasks, the BSSA_S3_CP variant is employed to be further compared with other well-regarded algorithms in the next subsection.

6.4. Comparison with other metaheuristics

In this section, efficiency of the BSSA_S3_CP strategy is investigated in comparison with a number of well-established metaheuristics in the field. For this purpose, the binary bGWO [74], BGSA [70], and BBA [75] algorithms are considered here to verify the performance of the proposed BSSA_S3_CP technique. The experiments performed according to a fair and same computing condition for all algorithms. Table 20 presents the detailed parameter settings for utilized methods.

Table 20: Parameter settings

Algorithm	**Parameter**	**Value**
GWO	a	[2 0]
BA	Q_{min} Frequency minimum	0
	Q_{max} Frequency maximum	2
	A Loudness	0.5
	r Pulse rate	0.5
GSA	G_0	100
	α	20

Table 21 reflects the average fitness results obtained by the proposed BSSA-based algorithm against other optimizers. Tables 22 and 23 also report the average classification accuracy, and the number of selected features together with the F-test ranking and STD values for all techniques.

From the results in Table 21, it can be recognized that the developed BSSA_S3_CP can surpass other peers on 82% of the datasets. Regarding the overall ranks, after the BSSA_S3_CP, which is the ranked one, the second best approaches are bGWO and BGSA, which each of which outperformed other contestants on two datasets. Based on STD values, the proposed BSSA_S3_CP has attained better fitness results with preferable STD values compared to other competitors in majority of datasets. The reason is that the BSSA_S3_CP still inherits all the advantages of the basic SSA over other optimizers such as its satisfactory LO escaping capacity. In addition, it has an advanced exploration capability due to the used crossover between salps, which boost its exploration tendency over the search when it is required and in the next phase, it can effectively focus on the vicinity of explored food source (leading salp), mainly, during the last iterations. Hence, it has established a more stable balance between the exploration and exploitation tendencies, which its effect can be detected in the improved fitness results of BSSA_S3_CP compared to the bGWO, BGSA, and BBA optimizers.

The results of Table 22 indicate that the proposed BSSA_S3_CP provides the best accuracies compared to the bGWO, BGSA, and BBA on 86% of the datasets. Regarding

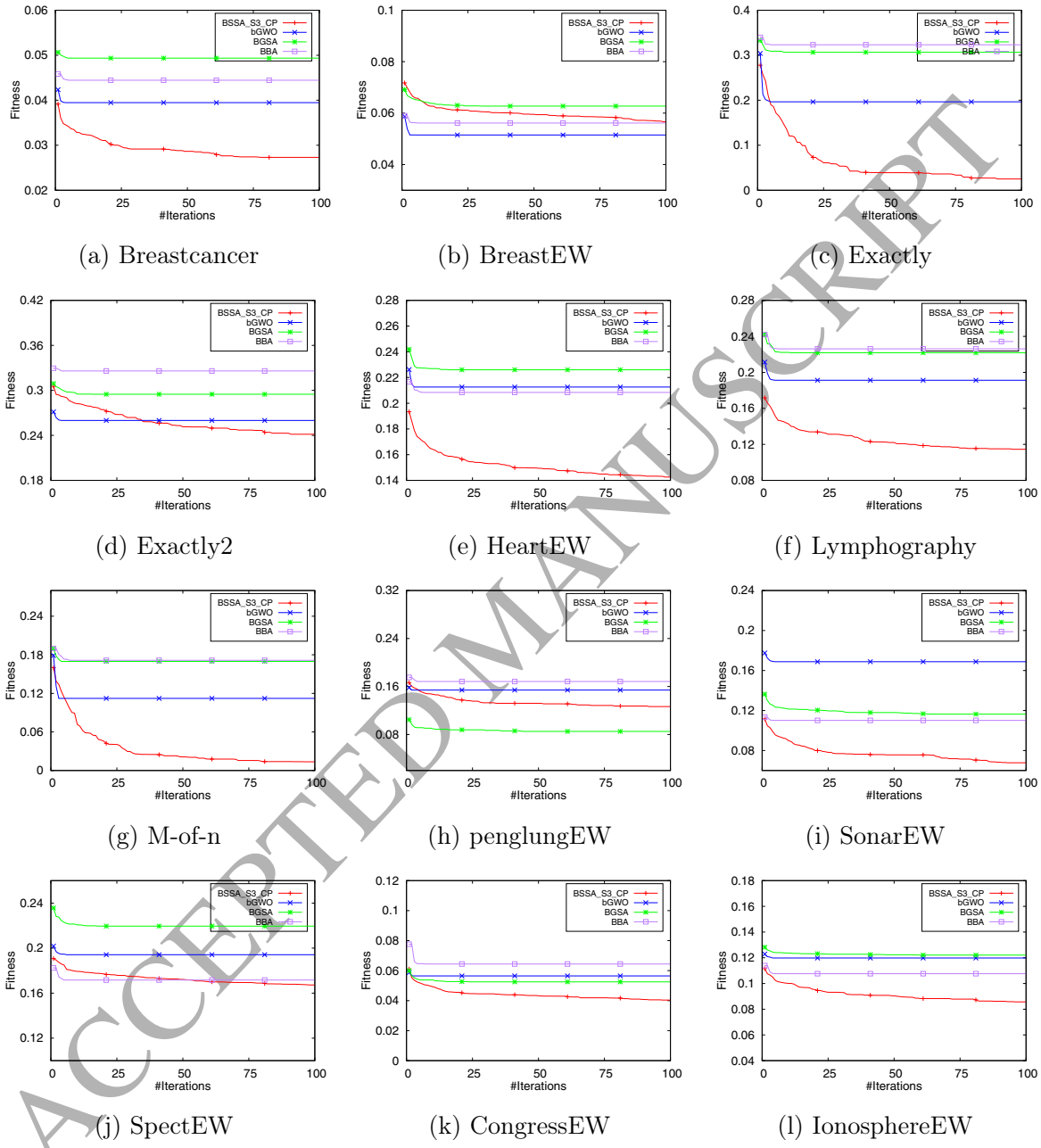
Table 21: Comparison between the BSSA_S3_CP and other metaheuristics based on the average fitness results.

	BSSA_S3_CP		bGWO		BGSA		BBA	
Benchmark	AVG	STD	AVG	STD	AVG	STD	AVG	STD
Breastcancer	**0.0273**	0.0006	0.0395	0.0031	0.0494	0.0034	0.0444	0.0047
BreastEW	0.0566	0.0033	**0.0515**	0.0069	0.0627	0.0057	0.0561	0.0062
Exactly	**0.0251**	0.0254	0.1965	0.0766	0.3066	0.0593	0.3233	0.0745
Exactly2	**0.2415**	0.0197	0.2599	0.0192	0.2949	0.0241	0.3259	0.0167
HeartEW	**0.1426**	0.0074	0.2126	0.0170	0.2260	0.0214	0.2084	0.0147
Lymphography	**0.1146**	0.0108	0.1912	0.0281	0.2218	0.0215	0.2262	0.0237
M-of-n	**0.0136**	0.0136	0.1122	0.0415	0.1697	0.0625	0.1714	0.0562
penglungEW	0.1266	0.0134	0.1541	0.0130	**0.0851**	0.0002	0.1683	0.0169
SonarEW	**0.0678**	0.0095	0.1688	0.0159	0.1164	0.0148	0.1101	0.0209
SpectEW	**0.1673**	0.0044	0.1941	0.0136	0.2196	0.0241	0.1716	0.0119
CongressEW	**0.0404**	0.0037	0.0565	0.0109	0.0525	0.0083	0.0644	0.0147
IonosphereEW	**0.0857**	0.0080	0.1198	0.0089	0.1221	0.0104	0.1076	0.0118
KrvskpEW	**0.0410**	0.0058	0.0730	0.0150	0.0966	0.0473	0.1174	0.0468
Tic-tac-toe	**0.1844**	0.0000	0.2512	0.0322	0.2514	0.0237	0.2568	0.0237
Vote	**0.0514**	0.0057	0.0603	0.0103	0.0731	0.0109	0.0712	0.0130
WaveformEW	**0.2695**	0.0071	0.2825	0.0073	0.3073	0.0140	0.3037	0.0135
WineEW	**0.0115**	0.0057	0.0467	0.0117	0.0542	0.0151	0.0365	0.0130
Zoo	**0.0042**	0.0004	0.0317	0.0085	0.0653	0.0078	0.0415	0.0149
clean1	0.1248	0.0041	**0.0987**	0.0062	0.1058	0.0104	0.1559	0.0130
semeion	**0.0255**	0.0014	0.0356	0.0026	0.0337	0.0020	0.0334	0.0026
Colon	0.3163	0.0185	0.3405	0.0217	**0.2370**	0.0143	0.2786	0.0352
Leukemia	**0.0166**	0.0247	0.1197	0.0162	0.1599	0.0135	0.0845	0.0229
Ranking (W|T|L)	**18|0|4**		2|0|20		2|0|20		0|0|22	
Overall Ranking (F-Test)	**1.3636**		2.5		3.1818		2.9545	

the rates of BBA, the BSSA_S3_CP can obtain superior rates on a11 100% of cases. The maximum and minimum rates have reached by the BSSA_S3_CP are 100% and 69% on Zoo and Colon problems, respectively. For M-of-n dataset, the BSSA_S3_CP have attained accuracy of 100%, while bGWO has not gone higher than the accuracy of 89%, which this fact affirms the improved efficiency of the proposed BSSA-based optimizer. The proposed BSSA_S3_CP has also found satisfactory solutions with acceptable SD values.

From Table 23, it seems that the BBA technique has a better performance on 82% of the datasets. The proposed BSSA_S3_CP can reveal the best efficacy in dealing with 18% of problems: Exactly2, HeartEW, CongressEW, and Vote.

The convergence curve of the proposed algorithm is compared to other competitors in Figs. 5 and 6. Inspecting the figures, it is seen that the BSSA_S3_CP can outperform all algorithms in dealing with 17 datasets. It is detected that the BSSA_S3_CP can reveal an accelerated trend in solving all problems. Premature convergence can be observed in the behaviors of the bGWO, BBA and BGSA algorithms on a number of the datasets such as the Tic-tac-toe, Zoo, Exactly, SpectEW, and Vote datasets. Regarding the above-mentioned observations, it can be concluded that the new crossover-based operator have improved the capabilities of BSSA in maintaining a fine balance between the explorative and exploitative phases. Therefore, the premature convergence and inactivity problems of the algorithm are relieved noticeably compared to bGWO, BGSA, and BBA optimizers.



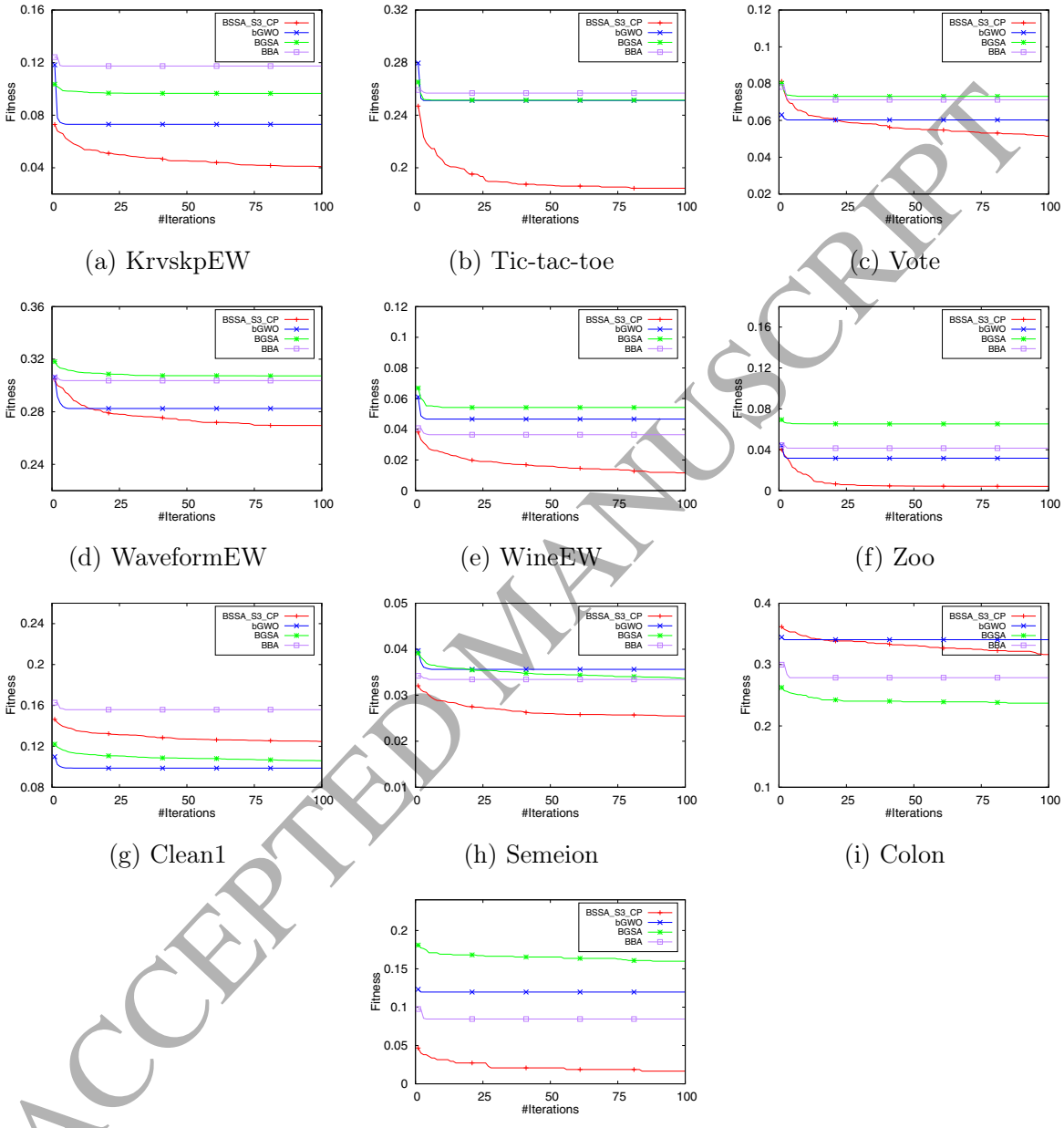
(a) Breastcancer (b) BreastEW (c) Exactly

(d) Exactly2 (e) HeartEW (f) Lymphography

(g) M-of-n (h) penglungEW (i) SonarEW

(j) SpectEW (k) CongressEW (l) IonosphereEW

Figure 5: Convergence curves for BSSA_S3_CP and other state-of-art methods for Breastcancer, BreastEW, Exactly, Exactly2, HeartEW, Lymphography, M-of-n, penglungEW, and SonarEW, SpectEW, CongressEW, and IonosphereEW datasets.



(a) KrvskpEW (b) Tic-tac-toe (c) Vote

(d) WaveformEW (e) WineEW (f) Zoo

(g) Clean1 (h) Semeion (i) Colon

(j) Leukemia

Figure 6: Convergence curves for BSSA_S3_CP and other state-of-art methods for KrvskpEW, Tic-tac-toe, Vote, WaveformEW, WineEW, Zoo, Clean1, Semeion, Colon, and Leukemia datasets.

Table 22: Comparison between the BSSA_S3_CP and other metaheuristics based on the average accuracy results.

	BSSA_S3_CP		bGWO		BGSA		BBA	
Benchmark	AVG	STD	AVG	STD	AVG	STD	AVG	STD
Breastcancer	**0.9768**	0.0010	0.9681	0.0023	0.9570	0.0039	0.9367	0.0305
BreastEW	0.9484	0.0035	**0.9544**	0.0071	0.9422	0.0057	0.9315	0.0144
Exactly	**0.9803**	0.0253	0.8095	0.0762	0.6971	0.0601	0.6099	0.0647
Exactly2	**0.7582**	0.0183	0.7431	0.0172	0.7061	0.0235	0.6282	0.0573
HeartEW	**0.8605**	0.0070	0.7916	0.0169	0.7770	0.0216	0.7538	0.0326
Lymphography	**0.8900**	0.0110	0.8131	0.0284	0.7811	0.0217	0.7014	0.0690
M-of-n	**0.9918**	0.0133	0.8941	0.0412	0.8352	0.0632	0.7219	0.0797
penglungEW	0.8775	0.0137	0.8495	0.0136	**0.9189**	0.0000	0.7946	0.0289
SonarEW	**0.9372**	0.0097	0.8356	0.0160	0.8875	0.0150	0.8439	0.0359
SpectEW	**0.8361**	0.0054	0.8097	0.0135	0.7826	0.0241	0.7998	0.0265
CongressEW	**0.9628**	0.0035	0.9476	0.0107	0.9512	0.0081	0.8717	0.0753
IonosphereEW	**0.9182**	0.0081	0.8847	0.0093	0.8813	0.0105	0.8765	0.0190
KrvskpEW	**0.9644**	0.0059	0.9339	0.0146	0.9081	0.0478	0.8164	0.0807
Tic-tac-toe	**0.8205**	0.0000	0.7538	0.0322	0.7526	0.0244	0.6653	0.0628
Vote	**0.9511**	0.0059	0.9438	0.0099	0.9313	0.0111	0.8511	0.0957
WaveformEW	**0.7335**	0.0069	0.7227	0.0067	0.6946	0.0142	0.6693	0.0326
WineEW	**0.9933**	0.0056	0.9596	0.0117	0.9509	0.0155	0.9187	0.0519
Zoo	**1.0000**	0.0000	0.9745	0.0091	0.9392	0.0079	0.8739	0.0949
clean1	**0.8796**	0.0042	0.9077	0.0062	0.8982	0.0106	0.8265	0.0208
semeion	**0.9799**	0.0015	0.9716	0.0030	0.9711	0.0021	0.9622	0.0063
Colon	0.6860	0.0188	0.6613	0.0220	**0.7656**	0.0145	0.6817	0.0376
Leukemia	**0.9889**	0.0253	0.8843	0.0164	0.8435	0.0136	0.8769	0.0289
Ranking (W|T|L)	**19|0|3**		1|0|21		2|0|20		0|0|22	
Overall Ranking (F-Test)	**1.2273**		2.1818		2.7727		3.8182	

6.5. Comparison with other algorithms reported in previous literature

In this part, the classification efficacy of the proposed BSSA_S3_CP is compared to the reported results for these datasets. Table 24 reveals the comparative classification rates of different approaches. The average classification rates of the BSSA_S3_CP is compared here to the reported performances of the GA and PSO algorithms in [27]. In addition, the results of the BSSA_S3_CP approach is also compared to the results of the bGWO1, bGWO2, GA, and PSO techniques reported in [46]. Note that the accuracies of the first and second GA and PSO optimizers are reported from [27], whereas the results of the rest of methods for the matching datasets are reported based on [46].

By comparing the results in Table 24, it can be seen that the accuracies of the BSSA_S3_CP proposed in this study is superior to those obtained from the past works on 86% of the datasets. It shows a substantial advantage over the binary GWO, PSO, and GA algorithms on the Lymphography, SonarEW, Tic-tac-toe, and Zoo datasets. The results of the BSSA_S3_CP are better than those of bGWO1, GA and PSO in [46] for all matching datasets. The BSSA_S3_CP technique can realize enhanced classification rates compared to the bGWO2 on around 94% of the matching datasets. It also surpasses the rates of GA and PSO from [27] on 100% and 90% of the problems, respectively.

The extensive experiments vividly demonstrated the merits of the proposed binary SSA algorithm combined with crossover scheme for dealing with feature selection tasks. The proposed algorithm outperformed various state-of-the-art approaches on majority of the selected datasets with different scales ranging from low-dimensional datasets like Breast

Table 23: Comparison between the BSSA_S3_CP and other metaheuristics based on average number of features.

	BSSA_S3_CP		bGWO		BGSA		BBA	
Benchmark	AVG	STD	AVG	STD	AVG	STD	AVG	STD
Breastcancer	3.8667	0.3457	7.1000	1.4468	6.0667	1.1427	**3.6667**	1.3730
BreastEW	16.7000	2.3364	19.0000	4.3072	16.5667	2.9790	**12.4000**	2.7618
Exactly	7.2000	0.6644	10.2333	1.6543	8.7333	1.0483	**5.7333**	1.8925
Exactly2	**2.7333**	2.3916	7.3333	4.1550	5.1000	2.1066	6.0667	2.3332
HeartEW	**5.8000**	1.4239	8.1667	2.0014	6.8333	1.3153	5.9000	1.6474
Lymphography	10.2667	1.9286	11.1000	1.9713	9.1667	1.8952	**7.8000**	2.2034
M-of-n	7.1000	0.6618	9.6333	0.9643	8.4667	1.4320	**6.1667**	2.0858
penglungEW	171.6000	9.9329	166.3333	28.2322	157.1667	7.7285	**126.1667**	15.6008
SonarEW	33.3667	2.8585	36.2333	8.6131	30.0333	3.6998	**24.7000**	5.3765
SpectEW	10.9333	3.5809	12.6333	2.4422	9.5333	2.3004	**7.9667**	2.2816
CongressEW	**5.7333**	1.3629	7.3000	2.1359	6.7667	2.4023	6.2333	2.0625
IonosphereEW	15.8667	2.5829	19.2333	5.0150	15.4000	2.5134	**13.4000**	2.5944
KrvskpEW	20.4667	2.5560	27.3667	3.3885	19.9667	2.1251	**15.0000**	2.8527
Tic-tac-toe	6.0000	0.0000	6.7000	1.3429	5.8667	1.1366	**4.7000**	1.4890
Vote	**4.8333**	1.4875	7.4000	2.2221	8.1667	1.8210	6.1333	2.1772
WaveformEW	22.9000	3.3255	31.9667	4.6125	19.9000	2.9167	**16.6667**	3.3045
WineEW	6.3333	0.9589	8.6000	1.7538	7.3667	1.0981	**6.0667**	1.7407
Zoo	6.7000	0.7022	10.3667	2.4842	8.1667	1.1769	**6.5667**	2.5008
clean1	92.1667	6.2427	121.2667	20.6914	83.7000	5.4212	**64.7667**	10.0161
semeion	147.5000	8.7168	200.1000	31.0221	133.5333	7.4219	**107.0333**	10.9465
Colon	1097.4333	44.7165	1042.1000	126.7211	995.8333	20.0208	**827.5000**	55.3707
Leukemia	3959.9333	530.6809	3663.7667	294.8722	3555.1333	39.7125	**2860.0000**	247.6421
Ranking (W|T|L)	4|0|18		0|0|22		0|0|22		18|0|4	
Overall Ranking (F-Test)	2.5455		3.8182		2.4091		1.2273	

Table 24: Comparison between the BSSA_S3_CP and other approaches from previous works based on the average accuracy results.

	BSSA_S3_CP	GA [27]	PSO [27]	bGWO1[46]	bGWO2 [46]	GA [46]	PSO [46]
Breastcancer	**0.9768**	0.957	0.949	0.976	0.975	0.968	0.967
BreastEW	**0.9484**	0.923	0.933	0.924	0.935	0.939	0.933
Exactly	**0.9803**	0.822	0.973	0.708	0.776	0.674	0.688
Exactly2	**0.7582**	0.677	0.666	0.745	0.750	0.746	0.730
HeartEW	**0.8605**	0.732	0.745	0.776	0.776	0.780	0.787
Lymphography	**0.89**	0.758	0.759	0.744	0.700	0.696	0.744
M-of-n	0.9918	0.916	**0.996**	0.908	0.963	0.861	0.921
penglungEW	0.8775	0.672	**0.879**	0.600	0.584	0.584	0.584
SonarEW	**0.9372**	0.833	0.804	0.731	0.729	0.754	0.737
SpectEW	**0.8361**	0.756	0.738	0.820	0.822	0.793	0.822
CongressEW	**0.9628**	0.898	0.937	0.935	0.938	0.932	0.928
IonosphereEW	**0.9182**	0.863	0.876	0.807	0.834	0.814	0.819
KrvskpEW	**0.9644**	0.940	0.949	0.944	0.956	0.920	0.941
Tic-tac-toe	**0.8205**	0.764	0.750	0.728	0.727	0.719	0.735
Vote	**0.9511**	0.808	0.888	0.912	0.920	0.904	0.904
WaveformEW	0.7335	0.712	0.732	0.786	**0.789**	0.773	0.762
WineEW	**0.9933**	0.947	0.937	0.930	0.920	0.937	0.933
Zoo	**1**	0.946	0.963	0.879	0.879	0.855	0.861
clean1	**0.8796**	0.862	0.845	-	-	-	-
semeion	**0.9799**	0.963	0.967	-	-	-	-
Colon	**0.686**	0.682	0.624	-	-	-	-
Leukemia	**0.9889**	0.705	0.862	-	-	-	-
Ranking (W|T|L)	**19|0|3**	0|0|22	2|0|20	0|0|18	1|0|17	0|0|18	0|0|18

cancer and Vote datasets, up to high-dimensional datasets like Leukemia. The main reason that this algorithm can perform well is behind the operators integrated in the algorithm. For one, the crossover operator can significantly change the position and behaviors of the leader salp. This results in driving the salp chain to different regions and promoting the exploratory tendencies. For another, the utilized S-shaped and V-shaped TFs can effectively map the continuous values to binary ones. Note that this does not mean that the proposed binary SSA algorithms are and will be the best option to tackle all classes of the optimization problems. According to NFL theorem [66], all algorithms perform equal when considering all types of optimization problems. Since the binary SSA approaches performed well on most of the FS problems, we suggest them to researchers in different fields particularly feature selection. The proposed algorithms have a high potential to provide very promising and/or superior results.

7. Conclusions and future directions

In this paper, an enhanced binary SSA-based optimizer with transfer functions and crossover scheme was proposed to tackle FS problems. The proposed techniques were tested on 22 well-regarded benchmark datasets. To detect the best TF for binary versions, the classification accuracy, features, and fitness measures was studied and statistical tests were also provided in detail. After the comparisons between the proposed versions, it was observed that the BSSA with S3-shaped TF and crossover outperform other hybrid variants. The efficacy of the BSSA_S3_CP method was compared to three state-of-the-art methods and several algorithms reported in previous works. The comparative evaluations of the BSSA_S3_CP against bGWO, BGSA, BBA, showed the superior efficiency of the proposed technique in terms of accuracy and fitness values for different FS problems.

For future research, interested researchers can investigate the efficacy of the proposed binary SSA in dealing with other datasets or machine learning tasks. The future work can also investigate the impact of other new S-shaped and V-shaped family of TFs on BSSA or other studied binary algorithms. Furthermore, the implementation of of slopes and saturations as new TFs for new metaheuristics, BSSA and other algorithms can be investigated in future researches.

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Appendix A

Table 25: Comparison between the BSSA with TFs approaches and the proposed method (with CP) based on the Best and Worst accuracy.

Benchmark	Stat.Measure	BSSA_S1	BSSA_S1_CP	BSSA_S2	BSSA_S2_CP	BSSA_S3	BSSA_S3_CP	BSSA_S4	BSSA_S4_CP	BSSA_V1	BSSA_V1_CP	BSSA_V2	BSSA_V2_CP	BSSA_V3	BSSA_V3_CP	BSSA_V4	BSSA_V4_CP
Breastcancer	Best	0.9771	0.9629	0.9571	0.9743	0.9743	0.9771	0.9686	0.9829	0.9686	0.9714	0.9714	0.9771	0.9686	0.9743	0.9686	0.9714
	Worst	0.9771	0.9571	0.9571	0.9629	0.9743	0.9743	0.9686	0.9829	0.9629	0.9686	0.9657	0.9686	0.9629	0.9714	0.9657	0.9629
BreastEW	Best	0.9544	0.9684	0.9649	0.9649	0.9719	0.9544	0.9614	0.9649	0.9649	0.9684	0.9719	0.9790	0.9684	0.9579	0.9614	0.9719
	Worst	0.9404	0.9544	0.9474	0.9404	0.9509	0.9404	0.9474	0.9544	0.9474	0.9544	0.9474	0.9579	0.9474	0.9298	0.9439	0.9544
Exactly	Best	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
	Worst	0.9600	0.9520	0.9420	0.9820	0.8600	0.9260	0.9260	0.9440	0.7760	0.8340	0.8280	0.7780	0.8100	0.8580	0.7720	0.8720
Exactly2	Best	0.7620	0.7700	0.7460	0.7700	0.7560	0.7680	0.7620	0.7380	0.7720	0.7400	0.7520	0.7540	0.7660	0.7400	0.7620	0.7540
	Worst	0.7120	0.7200	0.7200	0.7340	0.7560	0.7180	0.7360	0.7080	0.6920	0.7080	0.7080	0.7540	0.7500	0.7060	0.7060	0.7100
HeartEW	Best	0.8593	0.8370	0.8444	0.8444	0.8222	0.8667	0.8519	0.8519	0.8370	0.8370	0.8222	0.8444	0.8370	0.8444	0.8444	0.8370
	Worst	0.8370	0.8222	0.8074	0.8222	0.7926	0.8370	0.8222	0.8296	0.8000	0.8000	0.7852	0.8222	0.8148	0.8074	0.8000	0.8000
Lymphography	Best	0.8784	0.8514	0.8243	0.8649	0.8784	0.9054	0.8784	0.8919	0.8919	0.8649	0.8784	0.8919	0.8514	0.8378	0.8243	0.8784
	Worst	0.8514	0.8243	0.7973	0.8108	0.8243	0.8767	0.8243	0.8649	0.8378	0.8108	0.8243	0.8243	0.7973	0.7838	0.7703	0.8243
M-of-n	Best	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
	Worst	0.9760	0.9760	0.9860	0.9820	0.9360	0.9600	0.9640	0.9760	0.8520	0.9460	0.8840	0.9240	0.8880	0.8620	0.9320	0.9300
PenglungEW	Best	0.8649	0.9460	0.9189	0.8108	0.8649	0.8919	0.8649	0.9460	0.9460	0.8649	0.8919	0.9189	0.9189	0.9189	0.9189	0.8919
	Worst	0.8378	0.8919	0.8649	0.7838	0.7838	0.8649	0.8108	0.9189	0.9189	0.8108	0.8378	0.9189	0.8919	0.8649	0.8649	0.8649
SonarEW	Best	0.8846	0.9423	0.8942	0.9231	0.9231	0.9615	0.8942	0.9135	0.9231	0.9231	0.9519	0.9135	0.9231	0.9231	0.8750	0.9231
	Worst	0.8462	0.9135	0.8558	0.8846	0.8654	0.9231	0.8558	0.8750	0.8846	0.8750	0.9231	0.8942	0.8750	0.8846	0.8173	0.8846
SpectEW	Best	0.8358	0.8657	0.8806	0.8508	0.8881	0.8433	0.8582	0.8582	0.8433	0.8358	0.8657	0.8508	0.8657	0.8881	0.8433	0.8508
	Worst	0.8060	0.8508	0.8433	0.8284	0.8582	0.8209	0.8358	0.8209	0.8209	0.7836	0.8209	0.8060	0.8358	0.8582	0.8134	0.8134
CongressEW	Best	0.9679	0.9771	0.9725	0.9771	0.9725	0.9679	0.9771	0.9725	0.9633	0.9817	0.9908	0.9725	0.9771	0.9679	0.9817	0.9817
	Worst	0.9495	0.9587	0.9587	0.9633	0.9495	0.9541	0.9633	0.9541	0.9450	0.9633	0.9679	0.9495	0.9541	0.9495	0.9633	0.9541
IonosphereEW	Best	0.9148	0.8807	0.9318	0.9375	0.9432	0.9375	0.9091	0.9205	0.9489	0.9205	0.9602	0.9205	0.9602	0.9318	0.9261	0.9205
	Worst	0.8977	0.8523	0.9148	0.9205	0.9148	0.9034	0.8750	0.8921	0.9205	0.8977	0.9148	0.8807	0.9375	0.8977	0.8864	0.8977
KrvskpEW	Best	0.9718	0.9731	0.9775	0.9743	0.9637	0.9737	0.9700	0.9769	0.9687	0.9743	0.9675	0.9568	0.9668	0.9731	0.9693	0.9681
	Worst	0.9543	0.9612	0.9625	0.9537	0.9481	0.9493	0.9499	0.9481	0.9368	0.9337	0.9312	0.9293	0.9318	0.9343	0.9387	0.9399
Tic-tac-toe	Best	0.7871	0.7933	0.7933	0.7829	0.8100	0.8205	0.7808	0.7954	0.8121	0.7871	0.7912	0.7891	0.7954	0.8079	0.7975	0.7829
	Worst	0.7871	0.7724	0.7829	0.7662	0.7954	0.8205	0.7745	0.7850	0.7954	0.7829	0.7871	0.7808	0.7829	0.7871	0.7724	0.7599
Vote	Best	0.9667	0.9800	0.9600	0.9600	0.9667	0.9667	0.9800	0.9533	0.9467	0.9667	0.9533	0.9667	0.9600	0.9800	0.9667	0.9800
	Worst	0.9467	0.9467	0.9400	0.9467	0.9533	0.9400	0.9533	0.9400	0.9267	0.9467	0.9333	0.9467	0.9400	0.9600	0.9400	0.9600
WaveformEW	Best	0.7452	0.7440	0.7464	0.7540	0.7468	0.7520	0.7444	0.7496	0.7428	0.7432	0.7440	0.7424	0.7384	0.7436	0.7392	0.7392
	Worst	0.7304	0.7284	0.7200	0.7284	0.7204	0.7168	0.7220	0.7192	0.7128	0.7212	0.7156	0.7124	0.7044	0.7224	0.7116	0.7036
WineEW	Best	1.0000	1.0000	0.9663	0.9775	0.9775	1.0000	0.9888	0.9775	0.9888	0.9663	0.9888	0.9888	1.0000	1.0000	0.9888	0.9888
	Worst	0.9888	0.9888	0.9551	0.9663	0.9663	0.9888	0.9775	0.9663	0.9663	0.9551	0.9663	0.9775	0.9663	0.9663	0.9663	0.9663
Zoo	Best	0.9412	0.9216	0.9608	0.9608	1.0000	1.0000	0.9608	0.9804	0.9608	1.0000	0.9608	0.9608	0.9804	0.9608	0.9608	1.0000
	Worst	0.9216	0.8824	0.9608	0.9608	1.0000	1.0000	0.9412	0.9608	0.9412	0.9608	0.9608	0.9412	0.9412	0.9412	0.9608	1.0000
Clean1	Best	0.8571	0.9076	0.9076	0.9118	0.9034	0.8866	0.9160	0.9118	0.8824	0.9076	0.8992	0.9160	0.9034	0.9244	0.9034	0.8950
	Worst	0.8361	0.8782	0.8908	0.8908	0.8824	0.8740	0.8908	0.8866	0.8613	0.8782	0.8698	0.8866	0.8866	0.8908	0.8698	0.8698
Semeion	Best	0.9824	0.9787	0.9812	0.9762	0.9799	0.9824	0.9724	0.9774	0.9799	0.9799	0.9774	0.9812	0.9849	0.9749	0.9837	0.9849
	Worst	0.9762	0.9724	0.9724	0.9674	0.9749	0.9774	0.9649	0.9711	0.9737	0.9724	0.9699	0.9711	0.9774	0.9686	0.9762	0.9774
Colon	Best	0.8710	0.7742	0.7419	0.8710	0.8065	0.7097	0.7419	0.9032	0.8387	0.9032	0.9355	0.9032	0.8710	0.9355	0.8710	0.9355
	Worst	0.8387	0.7419	0.7097	0.8387	0.7742	0.6452	0.7097	0.8710	0.7419	0.7097	0.8065	0.7742	0.7742	0.8387	0.8065	0.5807
Leukemia	Best	0.9333	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.9333	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
	Worst	0.8667	0.9333	0.9333	1.0000	1.0000	0.9333	1.0000	0.8667	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.9333	0.9333

References

[1] L. Yu, H. Liu, Feature selection for high-dimensional data: A fast correlation-based filter solution, in: Proceedings of the 20th international conference on machine learning (ICML-03), pp. 856–863.

[2] H. Liu, H. Motoda, Feature Selection for Knowledge Discovery and Data Mining, Kluwer Academic Publishers, Boston, 1998.

[3] H. Liu, R. Setiono, Chi2: Feature selection and discretization of numeric attributes, 1995.

[4] J. Quinlan, Induction of decision trees, Machine learning 1 (1986) 81–106.

[5] J. Quinlan, C4. 5: programs for machine learning, Morgan kaufmann, 1993.

[6] M. Robnik-Łikonja, I. Kononenko, Theoretical and empirical analysis of relieff and rrelieff, Machine learning 53 (2003) 23–69.

[7] R. Kohavi, G. H. John, Wrappers for feature subset selection, Artificial intelligence 97 (1997) 273–324.

[8] E. Pashaei, N. Aydin, Binary black hole algorithm for feature selection and classification on biological data, Applied Soft Computing 56 (2017) 94–106.

[9] U. Fayyad, G. Piatetsky-Shapiro, P. Smyth, From data mining to knowledge discovery in databases, AI magazine 17 (1996) 37.

[10] I. Guyon, A. Elisseeff, An introduction to variable and feature selection, Journal of machine learning research 3 (2003) 1157–1182.

[11] D. Rodrigues, X.-S. Yang, A. N. De Souza, J. P. Papa, Binary flower pollination algorithm and its application to feature selection, in: Recent Advances in Swarm Intelligence and Evolutionary Computation, Springer, 2015, pp. 85–100.

[12] J. Kennedy, Swarm intelligence, in: Handbook of nature-inspired and innovative computing, Springer, 2006, pp. 187–219.

[13] J. Kennedy, R. Eberhart, A new optimizer using particle swarm theory, in: Micro Machine and Human Science, 1995. MHS '95., Proceedings of the Sixth International Symposium on, pp. 39–43.

[14] M. Dorigo, M. Birattari, T. Stutzle, Ant colony optimization, IEEE computational intelligence magazine 1 (2006) 28–39.

[15] S. Mirjalili, Dragonfly algorithm: a new meta-heuristic optimization technique for solving single-objective, discrete, and multi-objective problems, Neural Computing and Applications 27 (2016) 1053–1073.

[16] S. Mirjalili, A. Lewis, The whale optimization algorithm, Advances in Engineering Software 95 (2016) 51–67.

[17] A. A. Heidari, R. A. Abbaspour, A. R. Jordehi, An efficient chaotic water cycle algorithm for optimization tasks, Neural Computing and Applications 28 (2017) 57–85.

[18] A. A. Heidari, R. A. Abbaspour, A. R. Jordehi, Gaussian bare-bones water cycle algorithm for optimal reactive power dispatch in electrical power systems, Applied Soft Computing 57 (2017) 657–671.

[19] A. H. Gandomi, A. H. Alavi, Krill herd: A new bio-inspired optimization algorithm, Communications in Nonlinear Science and Numerical Simulation 17 (2012) 4831–4845.

[20] W.-T. Pan, A new fruit fly optimization algorithm: Taking the financial distress model as an example, Knowledge-Based Systems 26 (2012) 69–74.

[21] S. Mirjalili, S. M. Mirjalili, A. Lewis, Grey wolf optimizer, Advances in Engineering Software 69 (2014) 46–61.

[22] X.-S. Yang, Firefly Algorithms for Multimodal Optimization, Springer Berlin Heidelberg, Berlin, Heidelberg, pp. 169–178.

[23] E. Zorarpacı, S. A. Özel, A hybrid approach of differential evolution and artificial bee colony for feature selection, Expert Systems with Applications 62 (2016) 91–103.

[24] K. Sorensen, M. Sevaux, F. Glover, A history of metaheuristics, arXiv preprint arXiv:1704.00853 (2017).

[25] S. Mirjalili, A. H. Gandomi, S. Z. Mirjalili, S. Saremi, H. Faris, S. M. Mirjalili, Salp swarm algorithm: A bio-inspired optimizer for engineering design problems, Advances in Engineering Software (2017).

[26] S. Kashef, H. Nezamabadi-pour, A new feature selection algorithm based on binary ant colony optimization, in: Information and Knowledge Technology (IKT), 2013 5th Conference on, IEEE, pp. 50–54.

[27] S. Kashef, H. Nezamabadi-pour, An advanced aco algorithm for feature subset selection, Neurocomputing 147 (2015) 271–279.

[28] P. Shunmugapriya, S. Kanmani, A hybrid algorithm using ant and bee colony optimization for feature selection and classification (ac-abc hybrid), Swarm and Evolutionary Computation (2017).

[29] Y. Wan, M. Wang, Z. Ye, X. Lai, A feature selection method based on modified binary coded ant colony optimization algorithm, Applied Soft Computing 49 (2016) 248–258.

[30] P. Moradi, M. Gholampour, A hybrid particle swarm optimization for feature subset selection by integrating a novel local search strategy, Applied Soft Computing 43 (2016) 117–130.

[31] S. Gunasundari, S. Janakiraman, S. Meenambal, Velocity bounded boolean particle swarm optimization for improved feature selection in liver and kidney disease diagnosis, Expert Systems with Applications 56 (2016) 28–47.

[32] K. K. Bharti, P. K. Singh, Opposition chaotic fitness mutation based adaptive inertia weight bpso for feature selection in text clustering, Applied Soft Computing 43 (2016) 20–34.

[33] L. M. Abualigah, A. T. Khader, E. S. Hanandeh, A new feature selection method to improve the document clustering using particle swarm optimization algorithm, Journal of Computational Science (2017).

[34] Y. Lu, M. Liang, Z. Ye, L. Cao, Improved particle swarm optimization algorithm and its application in text feature selection, Applied Soft Computing 35 (2015) 629–636.

[35] R. Sheikhpour, M. A. Sarram, R. Sheikhpour, Particle swarm optimization for bandwidth determination and feature selection of kernel density estimation based classifiers in diagnosis of breast cancer, Applied Soft Computing 40 (2016) 113–131.

[36] F. G. Mohammadi, M. S. Abadeh, Image steganalysis using a bee colony based feature selection algorithm, Engineering Applications of Artificial Intelligence 31 (2014) 35–43.

[37] A. Moayedikia, R. Jensen, U. K. Wiil, R. Forsati, Weighted bee colony algorithm for discrete optimization problems with application to feature selection, Engineering Applications of Artificial Intelligence 44 (2015) 153–167.

[38] E. Zorarpacı, S. A. Özel, A hybrid approach of differential evolution and artificial bee colony for feature selection, Expert Systems with Applications 62 (2016) 91–103.

[39] S. Mirjalili, The ant lion optimizer, Advances in Engineering Software 83 (2015) 80–98.

[40] H. M. Zawbaa, E. Emary, B. Parv, Feature selection based on antlion optimization algorithm, in: Complex Systems (WCCS), 2015 Third World Conference on, IEEE, pp. 1–7.

[41] E. Emary, H. M. Zawbaa, A. E. Hassanien, Binary ant lion approaches for feature selection, Neurocomputing 213 (2016) 54–65.

[42] H. M. Zawbaa, E. Emary, B. Parv, M. Sharawi, Feature selection approach based on moth-flame optimization algorithm, in: Evolutionary Computation (CEC), 2016 IEEE Congress on, IEEE, pp. 4612–4617.

[43] A. A. Heidari, P. Pahlavani, An efficient modified grey wolf optimizer with lévy flight for optimization tasks, Applied Soft Computing 60 (2017) 115–134.

[44] A. A. Heidari, R. A. Abbaspour, Enhanced chaotic grey wolf optimizer for real-world optimization problems: A comparative study, in: Handbook of Research on Emergent Applications of Optimization Algorithms, IGI Global, 2018, pp. 693–727.

[45] H. Faris, I. Aljarah, M. A. Al-Betar, S. Mirjalili, Grey wolf optimizer: a review of recent variants and applications, Neural Computing and Applications (2017) 1–23.

[46] E. Emary, H. M. Zawbaa, A. E. Hassanien, Binary grey wolf optimization approaches for feature selection, Neurocomputing 172 (2016) 371–381.

[47] E. Emary, H. M. Zawbaa, C. Grosan, A. E. Hassenian, Feature subset selection approach by gray-wolf optimization, in: Afro-European Conference for Industrial Advancement, Springer, pp. 1–13.

[48] S. Mirjalili, Moth-flame optimization algorithm: A novel nature-inspired heuristic paradigm, Knowledge-Based Systems 89 (2015) 228–249.

[49] M. M. Mafarja, S. Mirjalili, Hybrid whale optimization algorithm with simulated annealing for feature selection, Neurocomputing (2017).

[50] A. K. Das, S. Das, A. Ghosh, Ensemble feature selection using bi-objective genetic algorithm, Knowledge-Based Systems 123 (2017) 116–127.

[51] L. Lu, J. Yan, C. W. de Silva, Feature selection for ecg signal processing using improved genetic algorithm and empirical mode decomposition, Measurement 94 (2016) 372–381.

[52] L. Lu, J. Yan, Y. Meng, Dynamic genetic algorithm-based feature selection scheme for machine health prognostics, Procedia CIRP 56 (2016) 316–320.

[53] S. Sarafrazi, H. Nezamabadi-pour, Facing the classification of binary problems with a gsa-svm hybrid system, Mathematical and Computer Modelling 57 (2013) 270–278.

[54] E. Rashedi, H. Nezamabadi-pour, Feature subset selection using improved binary gravitational search algorithm, Journal of Intelligent & Fuzzy Systems 26 (2014) 1211–1221.

[55] U. Mlakar, I. Fister, J. Brest, B. Potočnik, Multi-objective differential evolution for feature selection in facial expression recognition systems, Expert Systems with Applications 89 (2017) 129–137.

[56] M. Z. Baig, N. Aslam, H. P. Shum, L. Zhang, Differential evolution algorithm as a tool for optimal feature subset selection in motor imagery eeg, Expert Systems with Applications 90 (2017) 184–195.

[57] Z. Zainuddin, K. H. Lai, P. Ong, An enhanced harmony search based algorithm for feature selection: Applications in epileptic seizure detection and prediction, Computers & Electrical Engineering 53 (2016) 143–162.

[58] D. Rodrigues, L. A. Pereira, R. Y. Nakamura, K. A. Costa, X.-S. Yang, A. N. Souza, J. P. Papa, A wrapper approach for feature selection based on bat algorithm and optimum-path forest, Expert Systems with Applications 41 (2014) 2250–2258.

[59] M. Mafarja, I. Aljarah, A. A. Heidari, A. I. Hammouri, H. Faris, A. Al-Zoubi, S. Mirjalili, Evolutionary population dynamics and grasshopper optimization approaches for feature selection problems, Knowledge-Based Systems 145 (2018) 25 – 45.

[60] R. Falcon, M. Almeida, A. Nayak, Fault identification with binary adaptive fireflies in parallel and distributed systems, in: Evolutionary Computation (CEC), 2011 IEEE Congress on, IEEE, pp. 1359–1366.

[61] C. C. Ramos, A. N. Souza, G. Chiachia, A. X. Falcão, J. P. Papa, A novel algorithm for feature selection using harmony search and its application for non-technical losses detection, Computers & Electrical Engineering 37 (2011) 886–894.

[62] D. Rodrigues, L. A. Pereira, T. Almeida, J. P. Papa, A. Souza, C. C. Ramos, X.-S. Yang, Bcs: A binary cuckoo search algorithm for feature selection, in: Circuits and Systems (ISCAS), 2013 IEEE International Symposium on, IEEE, pp. 465–468.

[63] D. Rodrigues, L. A. Pereira, J. P. Papa, C. C. Ramos, A. N. Souza, L. P. Papa, Optimizing feature selection through binary charged system search, in: International Conference on Computer Analysis of Images and Patterns, Springer, pp. 377–384.

[64] M. Dash, H. Liu, Feature selection for classification, Intelligent data analysis 1 (1997) 131–156.

[65] H. Liu, L. Yu, Toward integrating feature selection algorithms for classification and clustering, IEEE Transactions on knowledge and data engineering 17 (2005) 491–502.

[66] D. H. Wolpert, W. G. Macready, No free lunch theorems for optimization, IEEE transactions on evolutionary computation 1 (1997) 67–82.

[67] F. Pernkopf, Bayesian network classifiers versus selective k-nn classifier, Pattern Recognition 38 (2005) 1–10.

[68] S. Mirjalili, A. Lewis, S-shaped versus v-shaped transfer functions for binary particle swarm optimization, Swarm and Evolutionary Computation 9 (2013) 1–14.

[69] J. Kennedy, R. C. Eberhart, A discrete binary version of the particle swarm algorithm, in: Systems, Man, and Cybernetics, 1997. Computational Cybernetics and Simulation., 1997 IEEE International Conference on, volume 5, IEEE, pp. 4104–4108.

[70] E. Rashedi, H. Nezamabadi-Pour, S. Saryazdi, Bgsa: binary gravitational search algorithm, Natural Computing 9 (2010) 727–745.

[71] M. Lichman, UCI machine learning repository, 2013.

[72] A. Moayedikia, K.-L. Ong, Y. L. Boo, W. G. Yeoh, R. Jensen, Feature selection for high dimensional imbalanced class data using harmony search, Engineering Applications of Artificial Intelligence 57 (2017) 38–49.

[73] E. Emary, H. M. Zawbaa, C. Grosan, Experienced gray wolf optimization through reinforcement learning and neural networks, IEEE transactions on neural networks and learning systems 29 (2018) 681–694.

[74] E. Emary, H. M. Zawbaa, A. E. Hassanien, Binary grey wolf optimization approaches for feature selection, Neurocomputing 172 (2016) 371–381.

[75] S. Mirjalili, S. M. Mirjalili, X.-S. Yang, Binary bat algorithm, Neural Computing and Applications 25 (2014) 663–681.